

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 An Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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Searcher: Jan

Searcher Phone #: 4498

Searcher Location: _____

Date Searcher Provided: 7/15/03

Date Completed: 7/15/03

Searcher Prep & Review Time: _____

Client Prep Time: 15

Final Time: + 10

Type of Search

NA Sequence (#) _____

AA Sequence (#) ☒

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Webis News _____

Sequence Systems ☒

WWW Internet _____

Other (specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:52:29 ; Search time 13.4523 Seconds
(without alignments)
1657.949 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260
Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALNHHYQORSLSLSPGK 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	1 GHNU	Ig gamma-1 chain C
2	1219	96.7	374	2 S69339	Ig heavy chain V r
3	1217	96.6	255	4 S31866	Ig gamma-1 chain C
4	1172	93.0	234	2 P10207	Ig gamma chain C r
5	1138	90.3	377	2 A23511	Ig gamma-3 chain C
6	1136	90.2	377	2 A60764	Ig gamma-3 chain C
7	1123	89.1	289	1 G3H0W1	Ig gamma-3 heavy C
8	1107	87.9	326	1 G2HU	Ig gamma-2 chain C
9	1097	87.1	327	1 G4HU	Ig gamma-4 chain C
10	883	70.1	323	1 GHRB	Ig gamma chain C r
11	868.5	68.9	328	2 I47160	Ig gamma 2b chain
12	868.5	68.9	328	2 I47159	Ig gamma 2b chain
13	868.5	68.7	277	2 I47162	Ig gamma 4 chain C
14	858	68.1	329	1 G2GP	Ig gamma-2 chain C
15	847.5	67.3	328	2 I47158	Ig gamma-1 chain C
16	840.5	66.7	328	2 I47161	Ig gamma 3 chain c
17	820	65.1	470	2 S22080	Ig heavy chain pre
18	813	64.5	333	2 P50018	Ig gamma-2b chain
19	812.5	64.5	329	1 G3MSC	Ig gamma-3 chain C
20	811.5	64.4	308	2 C30554	Ig heavy chain C r
21	811.5	64.4	472	2 S31459	Ig gamma-1 chain c
22	801.5	63.6	398	1 G3MSM	Ig gamma-3 chain C
23	794.5	63.1	444	2 P4436	Ig gamma-2 chain C
24	789.5	62.7	324	1 G1MS	monoclonal antibody
25	784.5	62.3	326	2 P50017	Ig gamma-1 chain C
26	784.5	62.3	333	1 G1MSM	Ig gamma-1 chain C
27	776.5	61.6	329	2 S00847	Ig gamma-2c chain
28	776	61.6	330	1 G2MSA	Ig gamma-2a chain
29	776	61.6	469	2 S37483	Ig gamma-2a chain

30	772	61.3	335	1 G2MSB	Ig gamma-2a chain
31	771	61.2	399	1 G2MSA	Ig gamma-2a chain
32	761	60.4	446	2 S40295	Ig gamma-2a chain
33	751.5	59.6	474	1 G2MS11	Ig gamma-2b chain
34	747.5	59.3	322	2 P50019	Ig gamma-2a chain
35	746.5	59.2	405	1 G2MSB	Ig gamma-2b chain
36	735	58.3	327	2 S06611	Ig gamma-2 chain C
37	731.5	58.1	475	2 S01321	Ig gamma-2b chain
38	669	53.1	180	2 I46732	Ig gamma heavy Cha
39	549	43.6	249	2 S69340	Ig heavy chain VHI
40	547	43.4	218	2 A36040	Ig heavy chain V-I
41	542	43.0	152	2 S14236	Ig gamma-1 chain C
42	366.5	29.1	572	2 B46529	Ig r heavy chain (
43	357	28.3	549	2 S04845	Ig heavy chain pre
44	353	28.0	343	2 S25644	Ig mu chain C regi
45	353	28.0	455	1 MHMS	Ig mu chain C regi

ALIGNMENTS

RESULT 1

GHNU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A9123; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <EIL>

A:Cross-references: EMBL:Z17370

A>Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A>Note: Lys330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Ohta, M.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <7AK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024; PMID:5483771

A:Accession: B90563

A:Contents: myeloma protein Eu

A:Molecule type: protein

A:Residues: 1-96, 'R', 98-135 <CUN>

A>Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2

A>Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponsig, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

1gen Primaerstruktur
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein N1e
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', '36-96', 'K', '98-115', 'Q', '117-197', 'D', '199-238', 'D', '240', 'L', '242-268', 'E', '27
A:Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOI, disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', '98-197', 'D', '199-238', 'E', '240', 'W', '242-266', 'D', '268-271', 'D', '273-330' <SCH
A:Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dieler, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbomide cleavage products, and the disulfide bridges
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Insertions: 99/1, 114/1, 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
E:20-85/Domain: immunoglobulin homology <IM1>
E:137-206/Domain: immunoglobulin homology <IM2>
E:243-310/Domain: immunoglobulin homology <IM3>
E:27-83, 114-204, 250-308/Disulfide bonds: #status experimental
E:103/Disulfide bonds: interchain (to light chain) #status experimental
E:109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
E:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.2%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 3.9e-86;
Matches 223; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDTHTCPCPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
99 EPKSCDTHTCPCPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158
|||||
61 NMVYDGEVHNHNAKTRPREQYNSTRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 120
|||||
159 NMVYDGEVHNHNAKTRPREQYNSTRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 218
|||||
121 ISRAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 180
|||||
219 ISRAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 278
|||||
181 PVLDSVGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNHYTQKSLSPGK 232
|||||
279 PVLDSVGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNHYTQKSLSPGK 330

RESULT 2
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilich, A.A.; Aucouturier, P.; Freund'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', '142-374' <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 96.7%; Score 1219; DB 2; Length 374;
Best Local Similarity 96.1%; Pred. No. 1.3e-85;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDTHTCPCPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
143 EPKSCDTHTCPCPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 202
|||||
61 NMVYDGEVHNHNAKTRPREQYNSTRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 120
|||||
203 NMVYDGEVHNHNAKTRPREQYNSTRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 262
|||||
121 ISRAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 180
|||||
263 ISRAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 322
|||||
181 PVLDSVGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNHYTQKSLSPGK 232
|||||
323 PVLDSVGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNHYTQKSLSPGK 374

RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
R:Fillipa, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene produc
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FTL>
A:Cross-references: EMBL:X70421; NID:933068; PIDN:CAA49866.1; PID:933069
C:Keywords: immunoglobulin
E:1-22/Region: Escherichia coli outer membrane protein A precursor
E:23-255/Region: human Ig gamma-1 chain C region

Query Match 96.6%; Score 1217; DB 4; Length 255;
Best Local Similarity 96.6%; Pred. No. 1.1e-85;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 EPKSCDTHTCPCPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
24 EPKSCDTHTCPCPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 83
|||||
61 NMVYDGEVHNHNAKTRPREQYNSTRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 120
|||||
84 NMVYDGEVHNHNAKTRPREQYNSTRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 143
|||||
121 ISRAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 180
|||||
144 ISRAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 203


```
QY      181 PVLDSVGSFFLYSKLTVDKSRPQGQNVFSCSYMHEALHNHHQQRLSLSPGK   232
        |||||
Db       204 PVLDSDGSEFLYSKLTVDKSRPQGQNVFSCSYMHEALHNHYTQKLSLSPGK   255
```

RESULT 4

Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
E:48-117/Domain: immunoglobulin homology <IMM>

Query Match	93.0%	Score 1172;	DB 2;	Length 234;
Best Local Similarity	95.6%	Pred No. 2.8e-82;		
Matches 215; Conservative		4; Mismatches 6;	Indels 0;	Gaps 0

```

OY      1  EPKSCDKNHTQPCPCAPARLGLGSPVLEPPKPKDMLMSIRTPVTCVWVDVSHNEDEYVF  60
Db      10  EPKSCDTHHTQPCPCAPARLGLGSPVLEPPKPKDMLMSIRTPVTCVWVDVSHNEDEYVF  69
OY      61  NMVYDGVGEVHNANKTKPREBOYNSTYRVVSVLTVLHONMNMNGKEYKCKVSNAKLPALIEKT  1200
Db      70  NMVYDGVGEVHNANKTKPREBOYNSTYRVVSVLTVLHODWLMNGKEYKCKVSNAKLPALIEKT  129
OY      121  ISKAVVOGREPOVYUPLPSPRDELTKNOVSLTCLVKGTFYSDIAVENESMGQRPNNKKTTP  180
Db      130  ISKAGGOREPOVYUPLPSPRDELTKNOVSLTCLVKGTFYSDIAVENESMGQRPNNKKTTP  189
OY      181  PVLDSVSGFELYSKLTVDKSRMOOGNVFSCSVNHEALHHNHYOORS  225
Db      190  PVLDSGSGFELYSKLTVDKSRMOOGNVFSCSVNHEALHHNHYOORS  234

```

RESULT 5

Ig gamma-3 chain C region (allotype G3m(b)) - human
 C.Species: Homo sapiens (man)
 C.Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_Change 23-Jul-1999
 C.Accession: A23511
 R.Hunk, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
 Nucleic Acids Res. 14, 1779-1789, 1986
 A.Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: CC
 A.Reference number: A23511; MUID:86148507; PMID:3081877
 A.Accession: A23511
 A.Molecule type: DNA
 A.Residues: 1-377 #HUC>
 A.Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g5770556
 C.Genetics:
 A.Gene: GDB:IGHG3
 A.Cross-references: GDB:119339; OMIM:147120
 A.Map position: 14q32.33-14q32.33
 A.Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 C.Superfamily: Immunoglobulin C Region; Immunoglobulin homology
 C.Keywords: Immunoglobulin
 E:20-85/Domain: Immunoglobulin homology <IM>

Query Match	90.3%	Score 1138	DB 2	Length 377
Best Local Similarity	89.7%	Pred. No. 2e-79		
Matches 208	Conservative	11	Mismatches	13
			Indels	0
			Gaps	0

QY 1 EPKSCKTHHTPPCPAPBELLGSPSVLEPPPKRDTLMI SRTEVTCVAVDVSHEDEPEYK 60
 ||||| :
 Db 146 EPKSCDTPPPCPRCPAPBELLGSPSVLEPPPKRDTLMI SRTEVTCVAVDVSHEDEPEYK 205

QY 61 NMYVDGEVHNHTKPREQYNSTIRVSVSLYLHQNMGKEKCKAVSNKALPAPIKT 120

QY	121	ISAAKQVPRPQVYLLTPPRDELTKNQVSLTFLVGFPPSDIAVEMESNGCPENNYKTP	160
QY	121	ISAAKQVPRPQVYLLTPPRDELTKNQVSLTFLVGFPPSDIAVEMESNGCPENNYKTP	160
Db	266	ISATKGPRPQVYLLTPPRDEMTKNQVSLTFLVGFPPSDIAVEMESNGCPENNYKTP	325
QY	181	PVLDSVGFPLYLTKLVDSKRMQOGNPFSCSYMHALLNNHQQKSLSPK	232
Db	326	PVLDSVGFPLYLTKLVDSKRMQOGNPFSCSYMHALLNNHQQKSLSPK	377

RESULT 6

Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
I:Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
E:20-85/Domain: immunoglobulin homology <IMM>

Query Match	90.2%	Score 1136	DB 2	Length 377
Best Local Similarity	89.7%	Pred No. 2.8e-79		
Matches 208	Conservative 11	Mismatches 13	Indels 0	Gaps 0

Qy	1	IPKSCDKNTNORPCARALELGGPSVFLPRPKDITMISRTPEVTCVVVDVSHEDDEHVK	60
Db	146	EPKSCDTPRPPRCAPRALELGGPSVFLPRPKDITMISRTPEVTCVVVDVSHEDDEVOF	205
Qy	61	NMYVGVGEVHNANKTKPREEOYNSTKRVKVSULITVLHONMMNGKEVKCKVSKALAPRIEKT	120
Db	206	KMYVGVGEVHNANKTKPREEOYNSTKRVKVSULITVLHODMNLNGKEVKCKVSKALAPRIEKT	265
Qy	121	ISKAKVQREPOVUTLPRSRDELTKNOVSLTCLVKGFYSDIAVMESKGOPENNYKTPR	180
Db	266	ISKTKGQREPOVUTLPRSRDEMTKNOVSLTCLVKGFYSDIAVMESKGOPENNYKTPR	325
Qy	161	PVLDSVGSPELYSKTLVYDCKRMQOGVSCSYMNEELAHNHOORSLISLSPGK	232
Db	326	PVLDSVGSPELYSKTLVYDCKRMQOGVSCSYMNEELAHNHFQKSLISLSPGK	377

RESULT 7

Ig gamma-3 heavy chain disease proteins human
 C.Species: Homo sapiens (man)
 C.Date: 31-Dec-1979 A92219 revision 23-Oct-1981 #text_change 16-Jul-1999
 C.Accession: A80442 A99219: A90198: A93915: A02149
 R.Frangiome, B., Roschewasser, E., Prellin, F., Franklin, E.C.
 Biochemistry 19, 4304-4308, 1980
 A.Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy chain disease protein
 A.Reference number: A90442; MUD:81021548; PMID:6774747
 A.Contents: heavy chain disease protein wis

A:Reference number: A92219; MUID:77118561; PMID:402363
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein A
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A>Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A>Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R.Wolfsenstein-Todell, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71: 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A:Reference number: A90198; MUID:77021516; PMID:823945
A:Contents: heavy chain disease protein ZUC, partial sequence corresponding to residues
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A>Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R.Alexander, A.; Steinmetz, M.; Barltanlt, D.; Frangione, B.; Franklin, E.C.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A:Reference number: A93915; MUID:82247835; PMID:6808505
A:Contents: heavy chain disease protein Omm
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70, 127-114, 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A>Note: a carboxyl-terminal Lys is removed posttranslationally
A>Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein Wis is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid
F:203-270/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

A:Note: Lys-33 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-119, 'Q', '21-57', 'Z', '59, 'A', '61-193, 'D', '195-325 <MAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Z1e
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', '26-57, 'EV', '60-85;133-171, 'ZZZ', '175, 'B', '177-193, 'D', '195-196, 'Q', '1
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Z1e
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
Submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Frangione, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4960472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (c
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
E:20-85/Domain: immunoglobulin homology <TM1>
E:133-202/Domain: immunoglobulin homology <TM2>
E:233-306/Domain: immunoglobulin homology <TM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:116/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	87.9%	Score 1107;	DB 1;	Length 326;
Best Local Similarity	88.4%	Pred. No. 3.8e-77;		
Matches 205;	Conservative 12;	Mismatches 11;	Indels 4;	Gaps 2;
1	EPKSCDKTHRCPPCPAPELLGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDDEVKR	60		
Db	99 ERKCCVE--CPCPAPR-VAGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDDEVKR	154		
QY	61 NWYVDGEVNAVTKRPEEDYNSTYRVVSVLT,HLQNMNNGKEKCKVSKALPAPIEKT	120		
	: : : : : : : : :			
Db	155 NWYVDGEVNAVTKRPEEDQFNSTFRVSVLT,VLVHQMNLGKKEVKCKVSKGLPAPIEKT	214		
QY	121 ISRAKVDREPOVYTLTPSRDELTKNOVSLTCLVKGSPDIAVEMSGCPENNTKTP	180		
	: : : : : : : :			

Db 215 ISKTGKQPREQVYTLPPSRREMTKNQVSLTCLVKGFFPSDIAVEMESNGPENNYKTPP 274
 QY 181 PVLDSVSFFLYSKLTVDKSRMOQGNFSCSVMEALHNHYQOQSLSPCK 232
 Db 275 PMLDSDSFFLYSKLTVDKSRMOQGNFSCSVMEALHNHYQOQSLSPCK 326

RESULT 9

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <EHL>

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: Protein

A:Residues: 1-30; 81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C:Superfamily: Immunoglobulin C region; Immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83;141-201;247-305/Disulfide bonds: #status predicted

F:106;109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 87.1%; Score 1097; DB 1; Length 327;

Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 11 CPCCPAPPELLGSPVFLPPKPKDTLMSRPEVTCVVVDVSHEDPEVKFMYVDGVEVH 70
 Db 106 CPSCPAPPELLGSPVFLPPKPKDTLMSRPEVTCVVVDVSHEDPEVKFMYVDGVEVH 165
 QY 71 NVKTRPREQYNTYRVVSVLTVLHQNMMNGKEYKCKVSNKALPAPIETISKAKVQPRE 130
 Db 166 NAKTRPREQFNSTYRVVSVLTVLHODMLNGKEYKCKVSNKALPAPIETISKAKGQPRE 225
 QY 131 POYVTLPPSRDELTKRNVSLCLVKGFFPSDIAVEMESNGPENNYKTPPVLDSVSFF 190
 Db 226 POYVTLPPSRDELTKRNVSLCLVKGFFPSDIAVEMESNGPENNYKTPPVLDSVSFF 285
 QY 191 LYSKLTVDKSRMOQGNFSCSVMEALHNHYQOQSLSPCK 232
 Db 286 LYSKLTVDKSRMOQGNFSCSVMEALHNHYQOQSLSPCK 327

RESULT 10

GHRB

Ig gamma chain C region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999

C:Accession: A91749; A90290; A93928; A90245; A94416; A02161

R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
 Immunogenetics 18, 387-397, 1983
 A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I hap
 A:Reference number: A91749; MUID:8403930; PMID:6313520

A:Accession: A91749

A:Molecule type: mRNA

A:Residues: 1-323 <BER>

A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-

R:Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunog

A:Reference number: A90290; MUID:76135469; PMID:1243651

A:Accession: A90290

A:Molecule type: Protein

A:Residues: 1-47; 'E', 49-71, 'PV', 72-128 <PRA>

R:Martens, C.L.; Moore, K.W.; Steimetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A:Title: Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy ch

A:Reference number: A93928; MUID:83299917; PMID:6193512

A:Accession: A93928

A:Molecule type: mRNA

A:Residues: 88-103; 'W', 105-143; 'E', 145-184; 'A', 186; 'E', 188-266 <MAR>

A:Cross-references: GB:M6426; NID:9165111; PID:AA31289.1; PID:9165112

A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic ma

R:Frutcher, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobul

A:Reference number: A90245; MUID:70110015; PMID:5461106

A:Accession: A90245

A:Molecule type: Protein

A:Residues: 132-143; 'E', 145-161 <FRU>

R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wikse

A:Reference number: A94416

A:Accession: A94416

A:Molecule type: Protein

A:Residues: 129-131;155-172; 'D', 174-184; 'A', 186; 'E', 188-200; 'D', 202-217; 'E', 219-232; 'A:Note: this has the e15 allotypic marker, 185-Ala

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-82/Domain: immunoglobulin homology <IM1>

F:130-199/Domain: immunoglobulin homology <IM2>

F:236-303/Domain: immunoglobulin homology <IM3>

F:173/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 70.1%; Score 883; DB 1; Length 323;

Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

QY 1 EPKSCDKTHT-----TC--PPCAPPELLGSPVFLPPKPKDTLMSRPEV 44
 Db 76 QPVTCNVAPPATNTKVDKTVAPSTCSKPTCPPELLGSPVFLPPKPKDTLMSRPEV 135
 QY 45 TCVVVDVSHEDPEVKFMYVDGVEVHNKTRPREQYNTYRVVSVLTVLHQNMMNGKEY 104
 Db 136 TCVVVDVSHEDPEVKFMYVDGVEVHNKTRPREQYNTYRVVSVLTVLHQNMMNGKEY 195
 QY 105 KCKVSNKALPAPIETISKAKVQPREQYNTYRVVSVLTVLHQNMMNGKEY 164
 Db 196 KCKVSNKALPAPIETISKAKVQPREQYNTYRVVSVLTVLHQNMMNGKEY 255
 QY 165 EMESNGPENNYKTPPVLDSVSFFLYSKLTVDKSRMOQGNFSCSVMEALHNHYQOQ 224
 Db 256 EMESNGPENNYKTPPVLDSVSFFLYSKLTVDKSRMOQGNFSCSVMEALHNHYQOQ 315
 QY 225 SLSPSPCK 232
 Db 316 SLSPSPCK 323

RESULT 11

A:Molecule type: protein
A:Residues: 69-133:312-329 <TUR>
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90384; MUID:75036072; PMID:4429665
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
R:Trischmann T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90385; MUID:75036073; PMID:4609467
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <R2>
R:Oliveira, B.; Iamm, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A:Reference number: A90354; MUID:71058474; PMID:4922544
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin C region, immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:143-202/Disulfide bonds: #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:47:19 ; Search time 7.24353 Seconds
(without alignments)
1328.428 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260

Sequence: 1 EPKSCDKTRHTCPAPPELL.....MHEALNNHYQORSLSPGK 232

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	330	1	GCL_HUMAN
2	1128	89.5	290	1	GCL_HUMAN
3	1107	87.9	326	1	GCL_HUMAN
4	1097	87.1	327	1	GCL_HUMAN
5	883	70.1	323	1	GC_RABIT
6	858	68.1	329	1	GC2_CAVPO
7	813	64.5	333	1	GCB_RAT
8	812.5	64.5	329	1	GCL_MOUSE
9	801.5	63.6	398	1	GCB_MOUSE
10	789.5	62.7	324	1	GCL_MOUSE
11	784.5	62.3	326	1	GCL_RAT
12	784.5	62.3	393	1	GCL_MOUSE
13	776.5	61.6	329	1	GCB_RAT
14	776	61.6	330	1	GCA_MOUSE
15	772	61.3	335	1	GCB_MOUSE
16	771	61.2	399	1	GCB_MOUSE
17	751.5	59.6	336	1	GCB_MOUSE
18	747.5	59.3	322	1	GCA_RAT
19	746.5	59.2	405	1	GCB_MOUSE
20	553	28.0	455	1	MOC_MOUSE
21	347	27.5	454	1	MOC_HUMAN
22	345	27.4	476	1	MOC_HUMAN
23	343	27.2	476	1	MOC_HUMAN
24	339	26.9	458	1	MOC_RABIT
25	334	26.5	429	1	EPIC_RAT
26	333	26.4	428	1	EPIC_HUMAN
27	332	26.3	421	1	EPIC_MOUSE
28	329	26.1	479	1	MOC_RABIT
29	325	25.8	450	1	MOC_CANFA
30	323	25.6	454	1	MOC_MESAU
31	318	25.2	457	1	MOC_SUNMU
32	297	23.6	438	1	HVC2_HETER
33	293.5	23.3	299	1	ALC_RABIT

34	287.5	22.8	438	1	HVC2_HETER	P23087 heterodontu
35	277.5	22.0	461	1	HVC2_HETER	P23088 heterodontu
36	276.5	21.9	393	1	HVC2_HETER	P23089 heterodontu
37	275.5	21.9	446	1	MOC_CHICK	P23084 gallus galli
38	267	21.2	370	1	HVC2_HETER	P23084 heterodontu
39	251.5	20.0	353	1	ALC1_HUMAN	P20758 heterodontu
40	251	19.9	353	1	ALC1_HUMAN	P20758 heterodontu
41	247	19.6	340	1	ALC2_HUMAN	P01876 homo sapien
42	243.5	19.3	344	1	ALC_MOUSE	P01878 mus musculu
43	236.5	18.8	481	1	MOC_MOUSE	P23735 ictalurus p
44	168.5	13.4	105	1	LAC1_MOUSE	P01843 mus musculu
45	167	13.3	104	1	LAC2_RAT	P20767 rattus norv

ALIGNMENTS

RESULT 1
ID GCL_HUMAN STANDARD: PRT: 330 AA.
AC P01857:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=7070269; PubMed=826475;
RA Ponsling H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL). AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN (7)
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT 19G1 immunoglobulin (myeloma protein Nle), I: purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN (8)
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Delsenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from *Staphylococcus*
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155,166,177,195,198,269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 DR EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A02146; GHHD.
 DR PDB: 1FC1; 15-JUL-92.
 DR PDB: 1FC2; 15-JUL-92.
 DR Genew: HGNC:5525; IGHG1.
 DR MIM: 147100; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_G1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; IgG1; 2.
 DR PROSITE: PS00290; IG_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 98 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 330
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126

FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT TURN 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770E106C2FA3D CRC64;
 Query Match 97.2%; Score 1225; DB 1; Length 330;
 Best Local Similarity 97.0%; Pred. No. 1e-93;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDDTHCPDAPAPELLGSPVFLPPPKKDTLMSRPEVTCVVDVSHDPEVKF 60
 DB 99 EPKSCDDTHCPDAPAPELLGSPVFLPPPKKDTLMSRPEVTCVVDVSHDPEVKF 158
 QY 61 NMVYDGVENVHAKKPREEOYNSTYRVSVLTVDHOMMNGKEKCKVSNALPAPIEKT 120
 DB 159 NMVYDGVENVHAKKPREEOYNSTYRVSVLTVDHOMMNGKEKCKVSNALPAPIEKT 218
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTPP 180
 DB 219 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTPP 278
 QY 181 PVLDSGSEFLYSKLTVDKSRMOGQNVFSCSVMEHALHNHYOQSLSPSK 232
 DB 279 PVLDSGSEFLYSKLTVDKSRMOGQNVFSCSVMEHALHNHYOQSLSPSK 330
 RESULT 2
 GC3_HUMAN STANDARD; PRT: 290 AA.
 AC P01860;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
 GN IGHG3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RX MEDLINE=81021548; PubMed=6774747;
 RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
 RT gamma 3 heavy-chain disease protein WIS.";
 RL Biochemistry 19:4304-4308(1980).

[illegible]

evolution of a gene family." ;
 Cell 29:671-679(1982).
 [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE-Fetal Liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes." ;
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications." ;
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Conneil G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein." ;
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains." ;
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOY).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins." ;
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2." ;
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G." ;
 RL Nature 221:145-148(1969).
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 CC -----
 DR EMBL: J00230; AAB59393.1; -.
 DR PIR: A02148; G2HU.
 DR HSSP: P01857; IFC1.
 DR Genew: HGNC:5526; IGHG2.
 DR MIM: 147110; -.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_cl.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 3.

DR SMART: SMO0410; IG-like: 1.
DR SMART: SMO0407; IG1: 2.
DR PROSITE; PS00290; IG_MHC; 2.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60
FT CONFLICT 109 109
SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
Query Match Best Local Similarity 87.9%; Score 1107; DB 1; Length 326;
Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;
1 EPKSCDTHHCPCPAPPELLGSGVFLPPPKPDKTMTSRPEVTCVVDVSHDPEYKF 60
Db 99 ERKCCVE---CPCPAPP-VAGSVFLPPPKPDKTMTSRPEVTCVVDVSHDPEYQF 154
61 NMVYDGEVHNVAKTRPREEOYNSTRVSVLTVLHONMMNGKEKCKVSNKALPAPIEKT 120
155 NMVYDGEVHNNAKTRPREEOGNSFTRVSVYLTVLHODLNGKEKCKVSNKGLPAPIEKT 214
QY 121 ISKAKVQPREQVYTLTPSRDELTKNOVSLTCLKGFPSDIAEWESNGPENNYKTPP 180
Db 215 ISKKGQPREQVYTLTPSRREMTKNVSLTCLKGFPSDIAEWESNGPENNYKTPP 274
QY 181 PVLDSVGSFFLYSKLTVDKSRMOQGNFSCSVMEHALHNHQKSLSTLSPK 232
Db 275 PMLDSGDSFFLYSKLTVDKSRMOQGNFSCSVMEHALHNHTQKSLSTLSPK 326
RESULT 4
GC4_HUMAN
AC GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1g gamma-4 chain C region.
GN IGHC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=6299662;
RX MEDLINE=83157104; PubMed=4192699;
RA Ellison J.M., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-184(1981).
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Plink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RL Blochem. J. 117:33-47(1970).
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DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; GAHU.
DR HSSP; P01842; 7FAB.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; .
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 87.1%; Score 1097; DB 1; Length 327;
Best Local Similarity 90.5%; Pred. No. 3.4e-83;
Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

OY 11 CPSPAPPELLGSPVFLPPPKDKTLMISRTPEVYCVVDVSHDEPEKFMVYDGVVH 70
DB 106 CPSPAPPELLGSPVFLPPPKDKTLMISRTPEVYCVVDVSHDEPEKFMVYDGVVH 165
OY 71 NVKTRPREQYNSTYRVSVLTJVLHONMNGEKYCKVSKALPAPIKTTSKAKVPRE 130
DB 166 NAKTRPREQYNSTYRVSVLTJVLHONMNGEKYCKVSKALPAPIKTTSKAKVPRE 225
OY 131 PÖVYTLPPSQEEMTKNOVSLTCLVKGFTPSDIAVEMESNGOPENNYKTTPEVLDGGSFF 190
DB 226 PÖVYTLPPSQEEMTKNOVSLTCLVKGFTPSDIAVEMESNGOPENNYKTTPEVLDGGSFF 285
OY 191 LYSKLTVDKSRMOQGNVFSQSVMEALHNHYQOQSLSLSPGK 232
DB 286 LYSRLTVDKSRMOQGNVFSQSVMEALHNHYQOQSLSLSPGK 327

RESULT 5

GC_RABIT

ID GC_RABIT

AC P01870;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma chain C region.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI-Taxid=9986;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=84030930; PubMed=6313520;

RA Bernstein K.E., Alexander C.B., Mage R.G.;

RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant

F-1 haplotype";

Immunogenetics 18:387-397(1983).

[2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT Immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).

RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).

[4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT Immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).

RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebowitz H.E., Fellows R.E. Jr., Delaney R.;
RL (in) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -I- MISCELLANEOUS: REF. 1 SEQUENCE HAS THE D12 ALLOTYPE MARKER.
CC 104-THR, AND THE E14 MARKER, 185-THR. REF. 3 HAS THE D11 AND E15
CC MARKERS AND REF. 5 THE E15 MARKER.

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DR EMBL; M16426; AAA31289.1; .
DR PIR; A02161; GHR.
DR HSSP; P01857; 1FCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPY (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 O -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> G (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8A110D579A8B CRC64;

Query Match 70.1%; Score 883; DB 1; Length 323;
Best Local Similarity 64.5%; Pred. No. 1.4e-65;
Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

OY 1 EPKSCDKTH-----TC--PPCAPPELLGSPVFLPPPKDKTLMISRTPEV 44
I : I : I

Db 76 QPVTCAHAPATNTKVDKTVAPSTCSKPTCPPELLGSPSVFIFPPKPKDTLMISRTPEV 135
 QY 45 TCVVVDVSHEDPEVKFMWYVDGVEVHNHKTREPOYNSTYRVSVLTVLTQHOMMNGKEY 104
 Db 136 TCVVVDVSDDEPEVQFTWYINNEQVRRAPRLRQEQNSTLRVSTLPLTHQDLRGEF 195
 QY 105 KCKVNNALPAPITKTSKAVQREPOVYTLPPSRDELTRKNQVSLTCLVKGFPSPDIAY 164
 Db 196 KCKVNNALPAPITKTSKAVQREPOVYTLPPSRDELTRKNQVSLTCLVKGFPSPDISV 255
 QY 165 EWSNGOPENNYKTTPTPLVDVSGSFPLYSKLTVDKSRMOQGNVSCSYMEHALNHNHVOOR 224
 Db 256 EWEKNGAEADNYKTTPTPLVDVSGSFPLYSKLTVDKSRMOQGNVSCSYMEHALNHNHVOOR 315
 QY 225 SLSSPSCK 232
 Db 316 SISRSPPCK 323

RESULT 6
 GC2_CAVPO STANDARD; PRT; 329 AA.
 AC P01862;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 19 gamma-2 chain C region.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 NCBI_Taxid=10141;
 RX MEDLINE=71058471; PubMed=5538606;
 RA Birstein B.K., Hussain Q.Z., Cedra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
 RT half-cysteine joining heavy and light chains.";
 RL Biochemistry 10:18-25(1971).
 RN 13
 RP SEQUENCE OF 69-133 AND 312-329.
 RX MEDLINE=71058486; PubMed=5538616;
 RA Turner K.J., Cedra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
 RT and hinge region cyanoogen bromide fragments.";
 RL Biochemistry 10:9-17(1971).
 RN 14
 RP SEQUENCE OF 134-226.
 RX MEDLINE=75036072; PubMed=4429665;
 RA Tracey D.E., Cedra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4796-4803(1974).
 RN 15
 RP SEQUENCE OF 227-311.
 RX MEDLINE=75036073; PubMed=4609467;
 RA Trischmann T.M., Cedra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4804-4811(1974).
 RN 16
 RP DISULFIDE BONDS.
 RX Oliveira B., Lamm M.E.; PubMed=4922544;
 RA "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
 RL Biochemistry 10:26-31(1971).
 CC 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
 CC 13 INBRED GUINEA PIGS.

DR PIR: A02151; G2AP.
 DR HSSP; P01842; 7EAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_1like.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00410; Ig_1like; 1.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 KW NON_TER
 FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 28 79 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 142 202 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 178 178
 FT DISULFID 248 308
 SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 68.1%; Score 858; DB 1; Length 329;
 Best Local Similarity 67.4%; Pred. No. 1.6e-63;
 Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

QY 1 EPKSCDKTHPCPCAPPELLGDSVFLFPPKPKDTLMISRTPEYTCVVVDVSHEDPEVKF 60
 Db 101 ZPBPC---TCPCPCPENIGSPVFIFPPKPKDTLMISRTPEYTCVVVDVSDDEPEVQF 156
 QY 61 NMWYDGVGVNHNHKTREPOYNSTYRVSVLTVLTQHOMMNGKEYKCKVNNALPAPITEKT 120
 Db 157 TWFDNKPVGNAETKRPVEQNTTFRVESVLPLOHOMLKEKCKVNNALPAPITEKT 216
 QY 121 ISKAVQREPOVYTLPPSRDELTRKNQVSLTCLVKGFPSPDIAYEWSNGOP--ENNYKT 178
 Db 217 ISKTKGAPRMPDVTLPSPSRDELTRKNQVSLTCLVKGFPSPDIAYEWSNGOP--ENNYKT 276
 QY 179 TTPVLVDVSGSFPLYSKLTVDKSRMOQGNVSCSYMEHALNHNHVOQRLSPG 231
 Db 277 TTPLEDADGVSFPLYSKLTVDKSRMOQGNVSCSYMEHALNHNHVOQRLSPG 329

RESULT 7
 GCB_RAT STANDARD; PRT; 333 AA.
 AC P20761;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 19 gamma-2B chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=101116;
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR: PS0018; PS0018.
 DR HSSP: P01842; 7EAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_1like.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00410; Ig_1like; 1.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region.
 KW NON_TER
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 80

```

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA: 36497 MW: 55F8B64D48D460A6 CRC64:

Query Match 64.5%; Score 813; DB 1; Length 333;
Best Local Similarity 63.6%; Pred. No. 8.1e-60;
Matches 145; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

OY 5 CDKTHCPCPAPELLGGSPVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNNYV 64
DB 106 CPTGCTHKCPVPELLGGSPVFIPEPKPKDILLISQNKATCVVVDVSEEDPDVQFSMFV 165
OY 65 DGEVHNKTKPREQYNTSTRVVSVLTVLIHONMNGEKYCKYSNKAIPAEIKTISK 124
DB 166 NNVEVHTAQTPREQYNTSTRVVSVLPIQHODMWSGKEFKCKVNNKALPSPIEKTSKP 225
OY 125 KVOPREPOVTLTPSRDELTKNOVSLTCLVKGFEVSDIAVEMESNGQPENNYKTTTPVLD 184
DB 226 KGLVKKPQVYVMGPTEBTEQVSLTCLSGFLPNDIGEVTSNGHIEKNTKTEPVMD 285
OY 185 SVGSEFLYSKLTVDKSRMOQGNVFCSVMHGALNNHYOORSLSPGK 232
DB 286 SDGSEFMYSKLNVERSRWDSPAFVCSVYHGLNHHNHEKSIISRPCK 333

RESULT 8
GC3M_MOUSE STANDARD: PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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CC -----
CC EMBL: J00451; -; NOT_ANNOTATED_CDS.
CC PIR: B02156; G3MSC.
CC HSSP: P01857; 1FC1.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003597; Ig_C1.
CC InterPro: IPR003600; Ig_Like.
CC Pfam: PF00047; Ig_3.
CC SMART: SM00407; IG_Like; 1.
CC SMART: SM00407; IG_C1; 2.
CC PROSITE: PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
CC Transmembrane; Alternative splicing.
CC NON_TER 1 1
CC DOMAIN 98 97 CH1.
CC DOMAIN 114 113 HINGE.
CC DOMAIN 223 CH2.

```

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FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA: 36228 MW: F45827174182BAD6 CRC64:

Query Match 64.5%; Score 812.5; DB 1; Length 329;
Best Local Similarity 64.7%; Pred. No. 8.8e-60;
Matches 145; Conservative 35; Mismatches 41; Indels 3; Gaps 1;

OY 12 PP--CPAPELLGGSPVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNNYV 68
DB 106 PPGSSCPGPNLTGGSPVFIPEPKPKDLMISRTKVTICVVVDVSEDDPDVHVSFVNKE 165
OY 69 VHNKTKPREQYNTSTRVVSVLTVLIHONMNGEKYCKYSNKAIPAEIKTISKARVQ 128
DB 166 VHTAMTQPREAQYNTSTRVVSVLPIQHODMWSGKEFKCKVNNKALPAPIEKTSKPKGRA 225
OY 129 REPQYTLTPSRDELTKNOVSLTCLVKGFEVSDIAVEMESNGQPENNYKTTTPVLDVGS 188
DB 226 QTPQYTLTPPREQYNTSTRVVSVLPIQHODMWSGKEFKCKVNNKALPAPIEKTSKPKGRA 285
OY 189 FFLYSKLTVDKSRMOQGNVFCSVMHGALNNHYOORSLSPGK 232
DB 286 YFLYSKLTVDKSRMOQGNVFCSVMHGALNNHYOORSLSPGK 329

RESULT 9
GC3M_MOUSE STANDARD: PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00451; AAB59655.1; -;
CC EMBL: V01526; CAA24767.1; ALU_SEQ.
CC PIR: A02155; G3MSM.
CC HSSP: P01857; 1FC1.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003597; Ig_C1.
CC InterPro: IPR003600; Ig_Like.
CC Pfam: PF00047; Ig_3.
CC SMART: SM00407; IG_Like; 1.
CC SMART: SM00407; IG_C1; 2.
CC PROSITE: PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
CC Transmembrane; Alternative splicing.

```

FT	NON_TER	1	97	CH1.
FT	DOMAIN	98	113	HINGE.
FT	DOMAIN	114	223	CH2.
FT	DOMAIN	224	327	CH3.
FT	TRANSMEM	346	362	POTENTIAL.
FT	DOMAIN	363	398	CYTOPLASMIC (POTENTIAL).
FT	CONFLICT	333	333	E -> G (IN REF. 2).
FT	CONFLICT	342	342	E -> Q (IN REF. 2).
FT	CONFLICT	388	388	P -> F (IN REF. 2).
SO	SEQUENCE	398 AA:	43929 MM:	CEFF264B50A41B95 CRC64:

Query Match 63.6%, Score 801.5; DB 1; Length 398;
Best Local Similarity 64.4%; Pred. No. 8.9e-59;
Matches 143; Conservative 35; Mismatches 41; Indels 3; Gaps 1.

QY	12	PP---CAPELLGSPVFLFPKPKDLMISRTPEVTCVVYDYSHEDEYKFNWYDGE	68
Db	106	PGSSGCEPGLNLGGSVFIPFPKPRDMLMISLTPKVTTCVVADVSDDPDVHVSFWDNKE	165
QY	69	VHNVKTRPREBOYNSTRVSVLTLYLHONMNGKREKCVSNKALPAPIETKISKAYOP	128
Db	166	VHTAMTQPREAOYNSTRFVSVALPILQDDMMKRGKFKCVNNKALPAPIETKISKARA	225
QY	129	REPOVYILPPERDELTKNQVSLTCLCYKGFYSDSIAVENESNGQPPNNKTTTPYLDVSGS	188
Db	226	QTPQVYIIPPREMOGSKKRVSLTCLVTFPESALISVEMERGELEODYKNTPTPIIDSDGT	285
QY	189	FFLXSKLTVDKSRMOQGNFCSVWHEALHNHYOORSLSP	230
Db	286	YFLSKLTVDIDSMWLGELTFCSVWHEALHNHYOORSLSP	327

RESULT 10
GCL_MOUSE
ID GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene";
RT Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RA MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid";
RT Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RA MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salsler W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain";
RT Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RA MEDLINE=78242288; PubMed=98524;
RA Adegbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a

[illegible]

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RESULT 11
GCL_RAT STANDARD: PRT: 326 AA.
AC P20759:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: P50017; PS0017.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_CL.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00407; IgCL1.2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 62.3%; Score 784.5; DB 1; Length 326;
Best Local Similarity 58.5%; Pred. No. 1.7e-57;
Matches 137; Conservative 46; Mismatches 42; Indels 9; Gaps 3;

QY 2 PKSCDKTHRCPCPAPELLG---PSVFLFPKPKDITLMISRTPEVTCVVVSHDEPV 58
DB 99 PRNCG--GDCKPC-----ICTGSEVSSVFIFPPKPKDVLITITLPAVTCVVDISODDEPV 152
QY 59 KENWYVDGEVHNVTKPREQYNSTYRVSVLTALHQMANGKEKCKVSKALPAPIE 118
DB 153 HESWFEVDVEHTAQTRPEEQFNSTFRVSSELPILHDMNGRFRCKVTAAPSPLE 212
QY 119 KTISSAKVQPREPOVYITLTPSRDELTKNOVSLTCLVKGYPEDIAVEMESNQPERNK 178
DB 213 KTISSKEGTEQVPHYITMSPKTEMTQNEVSITCMVKGYPEDIVEMQNGOPENYKN 272
QY 179 TPPEVDSVGSFPLYSKLVKVDKSRMOGANGFSCSVMEALHNHYOORSLSPGK 232
DB 273 TPPEVDSVGSFPLYSKLVKLVNKKERKMOGNGFTCTSVLHEGLHNHTEKSLSHSPGK 326

RESULT 12
GCL_MOUSE STANDARD: PRT: 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Coman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=679207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -! ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
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CC or send an email to license@sib.ch)
CC -----
DR EMBL: V00793; CAA24172.1; -
DR EMBL: V00793; CAA24173.1; -
DR EMBL: V00793; CAA24174.1; -
DR PIR: B02159; G1MSM.
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96446; Igh-4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_CL.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00407; IgCL1.2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174
FT DISULFID 244 302
N-LINKED (GLCNAC. . .)

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FT TRANSMEM 340 357 POTENTIAL.
 FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 393 AA; 43386 MW; 4ACC88343B7A1CE27 CRC64;
 Query Match 62.3%; Score 784.5; DB 1; Length 393;
 Best Local Similarity 58.2%; Pred. No. 2.2e-57;
 Matches 135; Conservative 47; Mismatches 41; Indels 9; Gaps 3;

QY 2 PKSCDKHTHTCPP--CPAPELIGGSPVFLFPKPKDTLMIISRTPEVTCVVDVSHDEPEVK 59
 DB 99 PRDGC-----CKPCICTVPEV---SSVFIFPPKPKDVLITLTPKVTGVVDVSDKDDPEVQ 151
 QY 60 FNNVVDVGVHNNVTKREDEYNSTRVSVLTVLHQNMMNGKEYCKVSKALPAPLEK 119
 DB 152 FSWFVDVGVHNTAQTQPREQFNSTFSPVSELPIMHDMVLGKBEKCVNSAPAPLEK 211
 QY 120 TISAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTT 179
 DB 212 TISTKGRKPKAPQYTTITPPKEQMAKDKVSLTCKMTDFEPEDITVEMQMGAPENNYKNT 271
 QY 180 PVLIDVSGSFPLYSKLTVDKSRMOQGVSCSVNHEALHNHYOORSLSLSPG 231
 DB 272 QPIMNTGSGYFVYSKLVNOKSNMEAGNTFTCSVLHEGLHNHHTKSLSHSPG 323

RESULT 13
 GCC_RAT
 ID P20762; STANDARD; PRT; 329 AA.
 AC P20762;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 19 gamma-2C chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88166903; PubMed=3127222;
 RA Brueggemann M., Delmastro-Galfrè P., Waldmann H., Calabi F.;
 RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
 RT region cDNA: extensive homology to mouse gamma 3.";
 RL Eur. J. Immunol. 18:317-319(1988).
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 CC -----
 DR EMBL: X07189; CAA30169.1; -
 DR PIR: S00847; S00847.
 DR HSSP: P01842; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00410; IgC1; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 FT Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DOMAIN 1 97 CHI.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 222 CH2.
 FT DOMAIN 223 329 CH3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 143 203
 FT DISULFID 249 307
 SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;
 Query Match 61.6%; Score 776.5; DB 1; Length 329;
 Best Local Similarity 61.6%; Pred. No. 8e-57;
 Matches 138; Conservative 42; Mismatches 41; Indels 3; Gaps 1;

QY 12 P--CPAPELIGGSPVFLFPKPKDTLMIISRTPEVTCVVDVSHDEPEVKFNNYGVGE 68
 DB 106 PPTICGCDNDLGRSPVFIFFPKPKDTLMTITLTPKVTGVVDVSEEDPDVQFSWFDVNR 165
 QY 69 VHNVTKPREQVNSTRVSVLTVLHQNMMNGKEYCKVSKALPAPLEKTSKARVQ 128
 DB 166 VFTAQTPHEEQNLGTRFVSVTLTIHQDMWSGKEFKCVNNKDLPSPIETKSKPRKA 225
 QY 129 REPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTTTPVLDSVG 188
 DB 226 RTFOVYTLPPREDDMSKNKVSLTQMTVSTFPAISVEMERNGELEDQYKNTLPVLDSDES 285
 QY 189 FFLYSKLTVDKSRMOQGVSCSVNHEALHNHYOORSLSLSPG 232
 DB 286 YFLYSKLTVDKSRMOQGVSCSVNHEALHNHYOORSLSLSPG 329

RESULT 14
 GCAA_MOUSE
 ID P01863; STANDARD; PRT; 330 AA.
 AC P01863;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 19 gamma-2A chain C region, A allele.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81076554; PubMed=6777755;
 RA Sikorav J.-L., Auffray C., Rougeon F.;
 RT "Structure of the constant and 3' untranslated regions of the murine
 RT Balb/c gamma 2a heavy chain messenger RNA.";
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81198976; PubMed=6262729;
 RA Yamawaki-Katsoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 RT and evolution of heavy chain genes: further evidence for intervening
 RT sequence-mediated domain transfer.";
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81223894; PubMed=6787604;
 RA Olio R., Auffray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic
 RT family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RX MEDLINE=74175517; PubMed=4831970;
 RA Bourgois A., Fougereau M., Rocca-Serra J.;
 RT "Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
 RT for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435(1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=73056887; PubMed=4565406;
 RA de Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma G2a


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RT Immunoglobulin. Identification of the disulfide bridges."
RL Eur. J. Biochem. 30:452-462(1972).
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CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; GZMSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
FT SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 61.6%; Score 776; DB 1; Length 330;
Best Local Similarity 62.9%; Pred. No. 8.9e-57;
Matches 141; Conservative 31; Mismatches 50; Indels 2; Gaps 1;

QY 11 CPE--CPAPELLGSPVFLFPKPKDITLMISRTPEVTCVYVDVSHEDPEVFNMYDGE 68
DB 107 CPECPAPNLGLGSPVFLFPKPKIDVLMISLSPVITCVYVDVSHEDDPDQISMFVNVE 166
QY 69 VHNKTKPREQYNSTYRVSVLTVLHONMNGKEVCKKVSNKALPADIETISKAKYOP 128
DB 167 VHTAQTQTHREDYNSTLTVSALPIOHODMWSGKEFKCKVNNKDLPAIERTISKPSV 226
QY 129 REPQVYTLPRPSRDLTKNOVSLTCLVGFYPSDIAVEMESNGQPENNKTPPVLDSDGS 188
DB 227 RAPQVYTLPRPEEHTKQVTLTCVYTPMPEDIVETWNTNGKTLNKTETPEVLDSDGS 286
QY 189 FFLYSKLTVDKSRMOQGNVFCQSYMHGALHNHYOQRLSLSPGK 232
DB 287 YFMYSKLVKLEKKNNWERNYSQSYVHEGLHNHHTTKSRPSPGK 330

RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2a chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RT "Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.,
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2a and IgG2b alleles of the mouse."

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RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dozin M.J., Lauwereys M., Stroosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms."
RT Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS:
CC -----
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CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; GZMSAB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT SEQUENCE 335 AA; 36596 MW; FA3382792CBBI3C6 CRC64;

Query Match 61.3%; Score 772; DB 1; Length 335;
Best Local Similarity 60.1%; Pred. No. 1.9e-56;
Matches 137; Conservative 39; Mismatches 52; Indels 0; Gaps 0;

QY 5 CDKTHCPCPAPELLGSPVFLFPKPKDITLMISRTPEVTCVYVDVSHEDPEVFNMY 64
DB 108 CPHRQVPCAPAPDLGLGSPVFLFPKPKIDVLMISLSPVITCVYVDVSHEDDPDQISMFV 167
QY 65 DGEVHNKTKPREQYNSTYRVSVLTVLHONMNGKEVCKKVSNKALPADIETISKAK 124
DB 168 NVEVHTAQTQTHREDYNSTLTVSALPIOHODMWSGKEFKCKVNNKDLPAIERTISK 227
QY 125 KQVREPQVYTLPRPSRDLTKNOVSLTCLVGFYPSDIAVEMESNGQPENNKTPPVLD 184
DB 228 RGPVAPQVYTLPRPAEHTKQVTLTCVYTPMPEDIVETWNTNGKTLNKTETPEVLD 287
QY 185 SVGSFFLYSKLTVDKSRMOQGNVFCQSYMHGALHNHYOQRLSLSPGK 232
DB 288 SGGSYFMYSKLVKLEKKNNWERNYSQSYVHEGLHNHHTTKSRPSPGK 335

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Search completed: July 15, 2003, 06:58:19
Job time : 8.24353 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:54:24 ; Search time 26.0767 Seconds
(without alignments)
1833.165 Million cell updates/sec

Title: US-09-847-208b-3
Perfect score: 1260
Sequence: 1 EPKSCDKHTHTCPAPAPPELL.....MHEALNNHYQQRSLSPGK 232

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1225	97.2	471 4 Q8TC77	Q8TC77 homo sapien
2	1225	97.2	701 4 Q96P08	Q96P08 homo sapien
3	1097	87.1	473 4 Q8TC63	Q8TC63 homo sapien
4	877.5	69.6	337 6 Q95M34	Q95M34 equus caball
5	798.5	63.4	463 11 Q8R3V9	Q8R3V9 mus musculu
6	795.5	63.1	469 11 Q99LC4	Q99LC4 mus musculu
7	791.5	62.8	437 11 Q9R1A4	Q9R1A4 mus musculu
8	782	62.1	473 11 Q9D8L4	Q9D8L4 mus musculu
9	772	61.3	468 11 Q99L31	Q99L31 mus musculu
10	752.5	59.7	473 11 Q99L25	Q99L25 mus musculu
11	752.5	59.7	474 11 Q91205	Q91205 mus musculu
12	752.5	59.7	474 11 Q8R3H6	Q8R3H6 mus musculu
13	347	27.5	375 4 Q9BS21	Q9BS21 homo sapien
14	347	27.5	597 4 Q9B0B8	Q9B0B8 homo sapien
15	347	27.5	597 4 Q96B89	Q96B89 homo sapien
16	347	27.5	597 4 Q9B010	Q9B010 homo sapien

17	343	27.2	613 11 Q8VCX7	Q8VCX7 mus musculu
18	337	26.7	588 4 Q8WUX4	Q8WUX4 homo sapien
19	337	26.7	613 4 Q96EY0	Q96EY0 homo sapien
20	337	26.7	613 4 Q8WUK1	Q8WUK1 homo sapien
21	337	26.7	614 4 Q96GA6	Q96GA6 homo sapien
22	337	26.7	618 4 Q96AA6	Q96AA6 homo sapien
23	272.5	21.6	684 13 Q90544	Q90544 glinglymocto
24	259	20.6	486 11 Q91207	Q91207 mus musculu
25	259	20.6	487 11 Q99KA4	Q99KA4 mus musculu
26	258	20.5	426 11 Q9PCD9	Q9PCD9 mus musculu
27	251.5	20.0	481 11 Q91WT3	Q91WT3 mus musculu
28	251.5	20.0	481 11 Q91WT1	Q91WT1 mus musculu
29	251.5	20.0	482 11 Q91X92	Q91X92 mus musculu
30	251.5	20.0	484 11 Q8VEA0	Q8VEA0 mus musculu
31	251.5	20.0	488 11 Q91WR1	Q91WR1 mus musculu
32	251.5	20.0	489 11 Q8VCX4	Q8VCX4 mus musculu
33	251	19.9	384 4 Q9UEB0	Q9UEB0 homo sapien
34	251	19.9	494 4 Q96K68	Q96K68 homo sapien
35	251	19.9	496 4 Q96KX8	Q96KX8 homo sapien
36	249.5	19.8	479 11 Q91WP5	Q91WP5 mus musculu
37	248.5	19.7	480 11 Q91XE1	Q91XE1 mus musculu
38	248	19.7	496 4 Q96DK0	Q96DK0 homo sapien
39	248	19.7	500 4 Q9BRV0	Q9BRV0 homo sapien
40	247	19.6	416 4 Q9NPP6	Q9NPP6 homo sapien
41	246	19.5	497 4 Q8WY24	Q8WY24 homo sapien
42	243.5	19.3	479 11 Q99M22	Q99M22 mus musculu
43	243.5	19.3	481 11 Q8VCV5	Q8VCV5 mus musculu
44	243.5	19.3	484 11 Q99LA6	Q99LA6 mus musculu
45	182.5	14.5	259 13 Q90530	Q90530 glinglymocto

ALIGNMENTS

RESULT 1
ID ID PRELIMINARY; PRT; 471 AA.
Q8TC77
AC Q8TC77;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAR24289.1; -
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF58660E CRC64;

Query Match 97.2%; Score 1225; DB 4; Length 471;
Best Local Similarity 97.0%; Pred. NO. 4.8e-108;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY	1	EPKSCDKHTHTCPAPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
DB	240	EPKSCDKHTHTCPAPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF	299
QY	61	NWYVDGVEVHNAVKTKRPREQNSYRYVSUTLVLHOMNMRKCKYKSNALPAPIEKT	120
DB	300	NWYVDGVEVHNAVKTKRPREQNSYRYVSUTLVLHOMNMRKCKYKSNALPAPIEKT	359
QY	121	ISKAKVQPREPQVYTLPPSRDELTKNOVSLCLVKGFPSPDAIEMESNGPENNYKTP	180
DB	360	ISKAKGPREPQVYTLPPSRDELTKNOVSLCLVKGFPSPDAIEMESNGPENNYKTP	419
QY	181	PVLDSVGSFYLTKLVKSRWQGNVFSVMHEALNNHYQQRSLSPGK	232

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Db      420 PVLSDSGSFLLSKLTVDKSRWQGNVFSQVMEHALHNHYTKSLSPGK 471
RESULT 2
ID      096P08      PRELIMINARY;      PRT:      701 AA.
AC      096P08;
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT      01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE      Factor VII active site mutant immunocoujugate.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21477448; PubMed=11593034;
RA      Hu 2., Garen A.;
RT      "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT      cells for immunotherapy in mouse models of prostate cancer.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR      EMBL; AF272774; AAK58686.1; -.
DR      InterPro: IPR000152; Asx_hydroxyl.
DR      InterPro: IPR000561; EGF-like.
DR      InterPro: IPR000742; EGF-2.
DR      InterPro: IPR001881; EGF_CA.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR001254; Ser_protease_Try.
DR      InterPro: IPR00294; VltK_dep_GLA.
DR      Pfam: PF00008; EGF_2.
DR      Pfam: PF00594; g1a; 1.
DR      Pfam: PF00047; Ig_2.
DR      Pfam: PF00089; trypsin; 1.
DR      SMART; SM00181; EGF_2.
DR      PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR      PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR      PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR      PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR      PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR      PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW      Hydrolase; Serine protease.
SQ      SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992E CRC64;

Query Match      97.2%; Score 1225; DB 4; Length 701;
Best Local Similarity 97.0%; Pred. No. 8.2e-108;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 EPPSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEVKF 60
      |||||||
DB      470 EPPSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEVKF 529
QY      61 NMYVDGEVYHNKTKPREEOYNSTYRVSVLTGLVHOMMNGKEKCKVSKALPAPEKTT 120
      |||||||
DB      530 NMYVDGEVYHNKTKPREEOYNSTYRVSVLTGLVHOMMNGKEKCKVSKALPAPEKTT 569
QY      121 ISRAKVOPEPPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPP 180
      |||||||
DB      590 ISRAKVOPEPPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPP 649
QY      181 PVLSDSGSFLLSKLTVDKSRWQGNVFSQVMEHALHNHYTKSLSPGK 232
      |||||||
DB      650 PVLSDSGSFLLSKLTVDKSRWQGNVFSQVMEHALHNHYTKSLSPGK 701

RESULT 3
ID      08TC63      PRELIMINARY;      PRT:      473 AA.
AC      08TC63;
DT      01-JUN-2002 (TReMBLrel. 21, Created)

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DT      01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT      01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE      Hypothetical 52.0 kDa protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98363416; PubMed=9717671;
RA      Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA      Leibold W., Radbruch A.;
RT      "Organization of the equine immunoglobulin heavy chain constant region
RT      genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL      Immunobiology 199:105-119(1998).
DR      EMBL; AJ30675; CAC44624.1; -.
DR      InterPro: IPR003006; Ig_MHC.
DR      Pfam: PF00047; Ig_2.
DR      PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
FT      NON TER
SQ      SEQUENCE 337 AA; 37438 MW; A60BF2B01DEDF1F6 CRC64;

Query Match      87.1%; Score 1097; DB 4; Length 473;
Best Local Similarity 90.5%; Pred. No. 7.1e-96;
Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY      11 CPSPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEKFMWYDGYEVH 70
      |||||||
DB      252 CPSPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEKFMWYDGYEVH 311
QY      71 NMYTKPREEOYNSTYRVSVLTGLVHOMMNGKEKCKVSKALPAPEKTTSKAKVQPRE 130
      |||||||
DB      312 NMYTKPREEOYNSTYRVSVLTGLVHOMMNGKEKCKVSKALPAPEKTTSKAKVQPRE 371
QY      131 PNYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLSDSGSF 190
      |||||||
DB      372 PNYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLSDSGSF 431
QY      191 LYSKLTVDKSRWQGNVFSQVMEHALHNHYTKSLSPGK 232
      |||||||
DB      432 LYSKLTVDKSRWQGNVFSQVMEHALHNHYTKSLSPGK 473

RESULT 4
ID      095M34      PRELIMINARY;      PRT:      337 AA.
AC      095M34;
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE      Immunoglobulin gamma 1 heavy chain constant region
DE      (Fragment).
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX      NCBI_TaxID=9796;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RL      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98363416; PubMed=9717671;
RA      Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA      Leibold W., Radbruch A.;
RT      "Organization of the equine immunoglobulin heavy chain constant region
RT      genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL      Immunobiology 199:105-119(1998).
DR      EMBL; AJ30675; CAC44624.1; -.
DR      InterPro: IPR003006; Ig_MHC.
DR      Pfam: PF00047; Ig_2.
DR      PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
FT      NON TER
SQ      SEQUENCE 337 AA; 37438 MW; A60BF2B01DEDF1F6 CRC64;

Query Match      69.6%; Score 877.5; DB 6; Length 337;
Best Local Similarity 67.7%; Pred. No. 3.3e-75;
Matches 157; Conservative 36; Mismatches 36; Indels 3; Gaps 2;

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QY	3	KSCQTHHCPCPAPPELLGGSVFLFPPKPKDITLMISTPEVTCVAVVSHDEPVRKFM	62
Db	107	KVCDMS-KCPKCAPPELLGGSVFLFPPNPKDITLITKPEVTCVAVVSOENPVRKFM	165
QY	63	VYDGEVHNVTKPREEOYNSTYRVSVLTVLHOMNMNGKEKCKVSNKALPAPIETIS	122
Db	166	YMDGEVATATTRKREGEFNSTYRVSVLTSLRQHOMWLSGKECKVNNQALPPIERIT	225
QY	123	KAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAEVESNGQP--ENNYKTP	180
Db	226	KTKGSGPOQVYVLAPHDELSTKSVSTCLVKGFPPEPINIEMWNSQPLETETYSTTO	285
QY	181	PVLDSVGSFELYSKLTVDKSRMOGNVSCSGMHEALNNHQQRSLSTSPGK	232
Db	286	AQODSDGSFYFLSKLSDVRNRMQOCTTTCGMHEALNNHYTKNVSNNPKG	337

RESULT 5

ID	Q8R3V9	PRELIMINARY:	PRT:	469 AA.
AC	Q8R3V9	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DE	Hypothetical 52.0 kDa protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	NCBI_TaxID=10090;			
RL	SEQUENCE FROM N.A.			
RU	Strausberg R.;			
DR	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
EMBL	BC024405; AAH24405.1; ..			
KW	Hypothetical protein.			
SO	SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;			

Query Match: 63.4%; Score 798.5; DB 11; Length 469;
 Best Local Similarity 59.2%; Pred. No. 1.6e-67;
 Matches 138; Conservative 45; Mismatches 41; Indels 9; Gaps 3

QY	2	PKSCDKHTHTCPP--CPAPPELLGGPVPFLFPPKPKDITLMISTPEVTCVAVVSHDEPVEK	59
Db	244	PRDGS---CKPCTCTPEV---SSVFLFPPKPKDITLITLTPKVTQVAVVDSKDDPEVQ	296
QY	60	FNMYVDGEVHNVTKPREEOYNSTYRVSVLTVLHOMNMNGKEKCKVSNKALPAPIEK	119
Db	297	FSWFVDGEVHTTAQTKPREEOFNSTYRSVSELPIMHOBWLNKEFKCRVNSAAPAPIEK	356
QY	120	TISAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAEVESNGQPENNYKTT	179
Db	357	TISKTKGPKPAQVYTLPPKPKQAKDKVSLTCLTDFPEEDITVEMQWNGQPAENYKNT	416
QY	180	PVLDSVGSFELYSKLTVDKSRMOGNVSCSGMHEALNNHQQRSLSTSPGK	232
Db	417	QPIMDTDSYFYFLSKLNVQKSNWMEAGNFTFCVLEGLNHNHTKSLSPGK	469

RESULT 6

ID	Q99LC4	PRELIMINARY:	PRT:	463 AA.
AC	Q99LC4	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
GN	Similar to RIKEN CDNA 1810060009 gene.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;				
RN	[1]			

[illegible]

Query Match	62.8%	Score 791.5	DB 11	Length 437
Best Local Similarity	58.4%	Pred. No. 6	9e-67	
Matches 136:	Conservative 47	Mismatches 41	Indels 9	Gaps 3
OY	2	PKSCDKTHTHCP--CPABELIGSPVFLFPPKPKDTLMIISKTPVEYCVVVDVSHEDPEVK	59	
Db	212	PRDGC---CKPCICTVPEV---SSVFIFPPKPKDVLITLTPKCCVVDVDSKDEPEVQ	264	
OY	60	FNWVVDGVEYVNVKTKPREEOYNSGRVSVSLTVLHOMWNGKEKCKVSKAKAPLPIEK	119	
Db	265	FSWVVDVEYVHTAQTQPREDFNSTERSVSLPIHOMLQKAEKCKVNSAAPLPIEK	324	
OY	120	TISKAKVQPREQYVTLPRSHDELLTKNOVSLTCLVYGPSDIANWESNGPENNKKYT	179	
Db	325	TISKTKGRPKAPQYVTLTPPRKQAKDKVSLTLCMTDFPEDFDIVEMQNGQPAENYKNT	384	
OY	180	PVYVDSGSPFLYKSLTVVDSRRMOQNGFSGSVNHEALNNHYQOQSLSLSGK	232	
Db	385	QPIMDTGISTFYVSKLVNOKSNMWRAGNFTQSVLHEGHHNNHTNNLSHSGK	437	

RESULT 8	09DBL4	PRELIMINARY;	PRF:	473 AA.
ID	Q9DBL4			
AC	Q9DBL4;			
DT	01-JUN-2001 (TREMblrel, 17, Created)			
DT	01-JUN-2001 (TREMblrel, 17, Last sequence update)			
DT	01-DEC-2001 (TREMblrel, 19, Last annotation update)			
DE	1810060009Rik protein.			
CN	IGH-1 OR 1810060009RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinaawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochaya H.,			
RA	Knehl P., Lewis S., Matsuo Y., Nkado I., Pesole G., Quackenbush J.,			
RA	Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gunstlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,			
RA	Nordone P., Ring B., Ringwald L., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyo-oka K., Wang K.H., Welfz C., Whitlaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuke S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
DR	EMBL AK007918. BAB25349.1; -			
DR	HSSP_P01842; 7FAB.			
DR	MGD: MG1:96443; Igh-1.			
DR	InterPro: IPR003599; Ig.			
DR	InterPro: IPR003597; Ig_C1.			
DR	InterPro: IPR003600; Ig_Like.			
DR	InterPro: IPR003008; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig_4.			
DR	SMART: SM00409; IG: 2.			
DR	SMART: SM00407; IG: 3.			
DR	SMART: SM00406; IGY: 1.			
DR	SMART: SM00410; IG_Like; 1.			
DR	PROSITE: PS00290; IG_MHC; UNKNOWN_1.			

QY	SEQUENCE	473 AA:	51699 MM:	9DED57A514475FBB	CNC64:
	Query Match	62.1%:	Score 782:	DB 11:	Length 473:
	Best Local Similarity	60.5%:	Pred. No. 6:	1e-66:	
	Matches 138:	Conservative 39:	Mismatches 51:	Indels 0:	Gaps 0:
QY	5	CDKHTTTPCPAPAPLLGGPSVFLEPPPKPKDMLSTRPEVTCVVVDVSHEDPEVKFNYY	64		
Db	246	CPPLKEPCPCAPAPLLTGGPSVFIEPPKIKDVLMLSTLSPMTCVVVDVEDDDPDQVISMFW	305		
QY	65	DGVEVHVWKKRPREQVNSYTRYVSVLTVLHQNMMNCKEYCKYSNKLAPRIETTSKA	124		
		: : : : : :			
Db	306	NNVEVHTAQQTREDYNSLTRVVSALPIQHQDMMSGEYFKCKNNRRLPSPITEYTSKP	365		
QY	125	KVQPREQVYTLPPSRDELTKNQVSLTCLGVGFPSDIAVMESENNGQPENNYKTTTPYVLD	184		
		: : : : : : : :			
Db	366	RGVPRAQVYVLPPLPAEEMTKKEESLTCLMIGFLPAETIAVDWTSNGRTQYKKNATVLD	425		
QY	185	SVGSFELYSLTVDKSRMGQGNVSCVGMHALLNNHQQRSLTSPCK	232		
		: : : :			
Db	426	SDGSYFHTSKLRYOKSTWKEKSLDAGSCVHEGGLNNHLTTKITSISLGR	473		

	RESULT	9
	099L31	
ID	Q99L31	PRELIMINARY; PRT; 468 AA.
AC	Q99L31;	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DE	Similar to RIKEN cDNA 1810060009 gene.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus.	
NCBI_taxonomy	taxid:10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Straussberg R.;	
RL	Submitted (FEB-2001).to the EMBL/GenBank/DDBJ databases.	
DR	EMBL: BC003878; AAH03878.1; .	
DR	HSSP: P01842; 7FAB.	
DR	InterPro: IPR003599; Ig.	
DR	InterPro: IPR003597; Ig_c1.	
DR	InterPro: IPR003600; Ig_1ike.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	InterPro: IPR003596; Ig_V.	
DR	Pfam: PF00047; Ig_3.	
DR	SMART: SM00409; IG; 2.	
DR	SMART: SM00407; IGc1; 3.	
DR	SMART: SM00406; IGV; 1.	
DR	SMART: SM00410; IG_1like; 1.	
DR	PROSITE, PS00290; IG_MHC; UNKNOWN_1.	
DR	SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;	
Query Match	61.3%; Score 772; DB 11; Length 468;	
Best Local Similarity	62.9%; Pred. No. 5,4e-65;	
Matches 141; Conservative 31; Mismatches 50; Indels 2; Gaps 1;		
QY	11 CPE--CPAPELLGGPSVFLEPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVE 68 : :	
Db	245 CPCKCCKPAENLLGGPSVFIFPPKIKDYMLMSLTSPMTCVVAVDSSEDDPDQISFWANNVE 304	
QY	69 VHNKVTKKRPEEQQNSNYRVAVSVLTVLVHOMNMNGKEKCYSNALPAPIETTSKAKVP 128 : : : : : : :	
Db	305 VLTAQQTQHREDNSTLRVAVSALPLIOHODMMSGKEFKCNKNALPAPIERTTISKPGSV 364	
QY	129 REPOVNTLPSPRDDELTKNQVSLTCLVKGFYPSDIAVMESNGOPENNYYKTTPVLDLVGS 188 : : : . :	
Db	365 RAPOQVYVLPPEPEEKMKKQVTLICMWTDPMEDIIVEMTNNGKTELNTYKITEFLVSDGS 424	
QY	189 FLYLSKLTVDKSRMQGCVNFSCGVMHDAALNNHYQQRSLSTSPCK 232 ::: :: : : :	
Db	425 YMYSKLRYAEKKWVERNSYSCVHEGLLNHHHTTSSFSRTPK 468	

RESULT 10
099L25 PRELIMINARY: PRT: 473 AA.
AC 099L25;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to Riken cDNA 1810606009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEb-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AHH03888.1; .
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003597; Ig.
DR InterPro; IPR003600; Ig_c1.
DR InterPro; IPR003006; Ig_like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 61.3%; Score 772; DB 11; Length 473;
Best Local Similarity 62.9%; Pred. No. 5.5e-65;
Matches 141; Conservative 31; Mismatches 50; Indels 2; Gaps 1;
QY 11 CPE--CPAPELLGSPVFLPPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNNYVDSGE 68
DB 250 CPCKCPAPNLGGPSVFLPPPKIKDVLMLISLPMVTCVVVDVSEDDVDQISMFVNNVE 309
QY 69 VHNKTKPREEQYNSTYRVSVLTVLHONMNGKEYKCKVSNKALPAPIETISKAKYOP 128
DB 310 VLTQOTQTHREDYNSTLRVSALPIQHDWMSGKEFKCKVNNKALPAPIETISKAKGSV 369
QY 129 REPQVYTLPRSDLTKNQVSLTCLVGFSPSDIAVEESGQEPNNKTPRPVLDVSGS 188
DB 370 RAPQVYVLPPEEETKQVLTCTGVDFMPEDIVETWNTNGKTELKNTPEVLDSDGS 429

QY 189 FFLYSKILTVDSKRMQGNVFSQVMEALHNHYOQRSLSLSPGK 232
DB 430 YFMFSKLRVEKKNNVERNYSQSVYHESLNHNHTKTSRTPGK 473
RESULT 11
091Z05 PRELIMINARY: PRT: 473 AA.
AC 091Z05;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN A0044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; .
DR MGD; MGI:2144967; A0044919.

DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 59.7%; Score 752.5; DB 11; Length 473;
Best Local Similarity 58.6%; Pred. No. 3.9e-63;
Matches 140; Conservative 36; Mismatches 56; Indels 7; Gaps 2;
QY 1 EPKSCDKT-HTCP-----CPAPELLGSPVFLPPPKPKDMLISRTPEVTCVVVDVSH 53
DB 235 EPSGPISTINCPCKCKCPAPNLBEGPSVFLPPPKIKVLMISLTPKTYCVVVDSE 294
QY 54 EDPVKFMVYDGVVHNVKTKPREQYNSTYRVSVLTVLHONMNGKEYKCKVSNKAL 113
DB 295 DDPOVQISMFVNNVEVHTAQOTQTHREDYNSTLRVSALPIQHDWMSGKEFKCKVNNKDL 354
QY 114 PAPIETISKAKVOPREPQVYTLPRSDLTKNQVSLTCLVGFSPSDIAVEESNGOPE 173
DB 355 PSLERTISKTKGLVRAPOVYTLPPPAQLSKDVSLCLVGFNPGDISVETWSNGHTE 414
QY 174 NNYKTPPVLDVSGSFLLYSKILTVDSKRMQGNVFSQVMEALHNHYOQRSLSLSPGK 232
DB 415 ENYKDTAVLDSDGSYFLYSKLDIKTSKWKETDPSQVRRHGLKNYLLKKTISRSPGK 473

RESULT 12
08R3H6 PRELIMINARY: PRT: 474 AA.
AC 08R3H6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; .
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 59.7%; Score 752.5; DB 11; Length 474;
Best Local Similarity 58.6%; Pred. No. 3.9e-63;
Matches 140; Conservative 36; Mismatches 56; Indels 7; Gaps 2;

QY 1 EPKSCDKT-HTCP-----CPAPELLGSPVFLPPPKPKDMLISRTPEVTCVVVDVSH 53
DB 236 EPSGPISTINCPCKCKCPAPNLBEGPSVFLPPPKIKVLMISLTPKTYCVVVDSE 295
QY 54 EDPVKFMVYDGVVHNVKTKPREQYNSTYRVSVLTVLHONMNGKEYKCKVSNKAL 113
DB 296 DDPOVQISMFVNNVEVHTAQOTQTHREDYNSTLRVSALPIQHDWMSGKEFKCKVNNKDL 355
QY 114 PAPIETISKAKVOPREPQVYTLPRSDLTKNQVSLTCLVGFSPSDIAVEESNGOPE 173
DB 356 PSLERTISKTKGLVRAPOVYTLPPPAQLSKDVSLCLVGFNPGDISVETWSNGHTE 415
QY 174 NNYKTPPVLDVSGSFLLYSKILTVDSKRMQGNVFSQVMEALHNHYOQRSLSLSPGK 232
DB 416 ENYKDTAVLDSDGSYFLYSKLDIKTSKWKETDPSQVRRHGLKNYLLKKTISRSPGK 474

RESULT 13
Q9BSZ1 PRELIMINARY: PRT: 375 AA.
ID Q9BSZ1

OY 199 KSRWQGNVFCVYHHEALHNNHYOORSLSLSPGX 232
: | | | | | : | |
Db 546 EEEWNTGETYTCVVAHEALPWRVTERVVDKSTGX 579

Search completed: July 15, 2003, 07:01:47
Job time : 30.0767 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:46:49 ; Search time 27.3185 seconds
(without alignments)
1131.621 million cell updates/sec

Title: US-09-847-208b-3
Perfect score: 1260
Sequence: 1 EPKSCDKHTHCPCPAPELL.....MHEALHNHYOORSLSLSPGK 232

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1982.DAT:*
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- 11: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1990.DAT:*
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- 21: /SIDS2/gcgdata/geneseq/genescp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/genescp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/genescp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	232	18	AAW26232
2	1225	97.2	232	21	AAW26290
3	1225	97.2	232	22	AAV72915
4	1225	97.2	232	22	AAAB8087
5	1225	97.2	232	23	AAE15347
6	1225	97.2	233	23	ABBO9463
7	1225	97.2	251	23	ABBA1490
8	1225	97.2	259	20	AA24154
9	1225	97.2	287	22	AAAB7590
10	1225	97.2	329	17	AAAB1806

11	1225	97.2	330	22	AAAB04071
12	1225	97.2	330	23	AAAB1641
13	1225	97.2	330	23	AAE21960
14	1225	97.2	330	23	ABBO5736
15	1225	97.2	330	23	AAW47836
16	1225	97.2	331	21	AAAY91106
17	1225	97.2	351	14	AAAR3685
18	1225	97.2	371	10	AAAP1918
19	1225	97.2	371	10	AAAP3558
20	1225	97.2	376	19	AAW60037
21	1225	97.2	379	19	AAW83962
22	1225	97.2	379	19	AAW49073
23	1225	97.2	388	23	ABBO7681
24	1225	97.2	396	18	AAW18574
25	1225	97.2	396	18	AAW18575
26	1225	97.2	400	21	AAV15123
27	1225	97.2	404	23	AAU97108
28	1225	97.2	423	21	AAAB28693
29	1225	97.2	424	16	AAW14764
30	1225	97.2	424	16	AAW14765
31	1225	97.2	426	21	AAAB28695
32	1225	97.2	435	13	AAAB6530
33	1225	97.2	437	18	AAW10532
34	1225	97.2	441	21	AAAB28692
35	1225	97.2	442	18	AAW10550
36	1225	97.2	445	20	AAW24153
37	1225	97.2	446	17	AAW05829
38	1225	97.2	447	20	AAV31669
39	1225	97.2	448	21	AAAB28694
40	1225	97.2	448	23	AAW49203
41	1225	97.2	449	14	AAAR3339
42	1225	97.2	449	19	AAW49816
43	1225	97.2	451	22	AAE12715
44	1225	97.2	451	23	AAU81014
45	1225	97.2	452	20	AAV30201

ALIGNMENTS

RESULT 1					
ID	AAW26232	standard; Protein: 232 AA.			
XX	AAW26232:				
AC	AAW26232:				
XX	16-MAR-1998 (first entry)				
DT	Human IgG1 hinge/Fc region.				
DE					
XX					
XX					
KW	Fusion protein: hydrophilic spacer; recombinant; expression system;				
KW	carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.				
OS	Homo sapiens.				
XX					
XX	WO9728272-A1.				
PN					
XX					
PD	07-AUG-1997.				
XX					
PF	31-JAN-1997; 97WO-US01470.				
XX					
PR	31-JAN-1996; 96US-0595043.				
PA	(TECH-) TECHNOLOGENE INC.				
XX					
PI	Sgarlato GD;				
XX					
DR	WPI; 1997-402624/37.				
DR	N-PSDB; AAT80158.				
XX					
PT	Recombinant protein expression system for fusion protein production				
PT	- useful for high quantity production of authentic recombinant				
PT	proteins				

Zcytor 10::IgG gam
Human IgG gamma 1
Human death domain
Human immunoglobul
Human Ig-gamma1 he
Human TR-Fc-delta-
Human kappa immuno
Sequence of the 11
linked human IgG
Antigenic peptide
Recombinant human
Recombinant human
MOG-Fc fusion prot
Aggrecanase artifl
Aggrecanase artifl
Porcine CTLA-4-19
Mouse MK61-human I
Fc-huA2P-1 (114-28
Human soluble kit
Fc-muA2P-1 (120-29
Sequence of one ch
Alpha-1-acid glyco
Fc-huA2P-1 (95-281
IgG1 polypeptide.
Bovine LOX-1 extra
Humanised ID10 ant
Human IgG1 chain C
Fc-muA2P-1 (95-291
Humanised monoclon
Completely humanis
Amino acid sequenc
Human recombinant
B7-related protein
Heavy chain sequen

xx Example 3; Page 133-134; 194pp; English.

cc A novel recombinant vector has been developed which comprises a
 cc nucleotide sequence encoding a fusion protein. The fusion protein
 cc comprises three domains joined together in order, from N-terminus to
 cc C-terminus, of a first domain comprising a protein of interest, a second
 cc domain comprising a hydrophilic spacer and an affinity domain, each
 cc the hinge/FC region of human IgG1, used in example 3 of the present
 cc invention. The recombinant vector is used for the production of
 cc authentic recombinant proteins of interest. The method of the invention
 cc is useful for the expression of fusion proteins capable of isolation by
 cc affinity chromatography in pro- or eukaryotic cells. This method allows
 cc for the efficient cleavage and generation of authentic proteins of
 cc interest that do not contain extraneous (i.e. non-naturally occurring)
 cc amino acids.

cc Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 18; Length 232;
 Best Local Similarity 97.0%; Pred. No. 2.1e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPAPELLGSPSVFLFPPPKPKDTLMISRTPEVTCVAVDVSHEDEPKVF 60
 Db 1 EPKSCDKTHTCPCPAPAPELLGSPSVFLFPPPKPKDTLMISRTPEVTCVAVDVSHEDEPKVF 60
 QY 61 NMVYDGEVHNHAKTRPREEOYNSTYRVSVLTVLHOMMNGKEYCKVSKALPAPIEKT 120
 Db 61 NMVYDGEVHNHAKTRPREEOYNSTYRVSVLTVLHOMMNGKEYCKVSKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGYGPPSDIAVEMESNGQPENNYKTP 180
 Db 121 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGYGPPSDIAVEMESNGQPENNYKTP 180
 QY 181 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVMEHALHNHYQKSLSPGK 232
 Db 181 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVMEHALHNHYQKSLSPGK 232

RESULT 2

AAB28690 ID AAB28690 standard; Protein: 232 AA.

AC AAB28690;

DF 14-FEB-2001 (first entry)

XX Human IgGammal hinge, CH2 and CH3 regions.

XX Human: AGP-1; type II transmembrane protein; cytosolic; antiviral;
 KW antiinflammatory; hepatotropic; antiatherosclerotic; anti-HIV; HIV;
 KW human immunodeficiency virus; apoptosis; proliferative disorder;
 KW cancer; hepatitis; acquired immunodeficiency syndrome; AIDS;
 KW autoimmune disorder; transplant rejection; cardiovascular disease;
 KW arteriosclerosis; IgGammal.

OS Homo sapiens.

XX WO200063253-A1.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08004.

XX 16-APR-1999; 99US-0293245.

XX (AMGE-) AMGEN INC.

XX Hsu H, Meng S;

XX WPI; 2000-665240/64.

xx Fusion protein of AGP-1 protein and an Fc region, used to treat
 PT proliferative disorders, immune disorders, and virally-induced
 PT disorders -

PS Claim 2; Fig 1; 93pp; English.

cc The present sequence was used in the production of AGP-1
 cc fusion proteins. AGP-1 is a type II transmembrane protein. The fusion
 cc proteins comprise an Fc immunoglobulin region fused to the N-terminal
 cc portion of the AGP-1 protein. The fusion proteins can be used to induce
 cc apoptosis in a tissue, and to treat proliferative disorders, immune
 cc disorders, or virally-induced disorders. The proliferative disorders
 cc include cancers, such as breast, prostate, lung or colon cancer. The
 cc viral infections include hepatitis, and acquired immunodeficiency
 cc syndrome (AIDS), and the immune disorders may be autoimmune disorders
 cc or transplant rejection. Cardiovascular diseases such as arteriosclerosis
 cc may also be treated. The AGP-1 containing fusion proteins have increased
 cc biological activity compared to the soluble AGP-1 proteins used in
 cc prior art therapies.

cc Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 21; Length 232;
 Best Local Similarity 97.0%; Pred. No. 2.1e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPAPELLGSPSVFLFPPPKPKDTLMISRTPEVTCVAVDVSHEDEPKVF 60
 Db 1 EPKSCDKTHTCPCPAPAPELLGSPSVFLFPPPKPKDTLMISRTPEVTCVAVDVSHEDEPKVF 60
 QY 61 NMVYDGEVHNHAKTRPREEOYNSTYRVSVLTVLHOMMNGKEYCKVSKALPAPIEKT 120
 Db 61 NMVYDGEVHNHAKTRPREEOYNSTYRVSVLTVLHOMMNGKEYCKVSKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGYGPPSDIAVEMESNGQPENNYKTP 180
 Db 121 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGYGPPSDIAVEMESNGQPENNYKTP 180
 QY 181 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVMEHALHNHYQKSLSPGK 232
 Db 181 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVMEHALHNHYQKSLSPGK 232

RESULT 3

AAV72915 ID AAV72915 standard; Protein: 232 AA.

AC AAV72915;

DT 13-JUN-2001 (first entry)

XX Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.

XX Human: fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KW hypercalcaemia; osteopenia; osteonerosis; rheumatoid arthritis;
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1;
 KW IgG1; periodontal.

XX Homo sapiens.

XX WO200118203-A1.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-US22797.

XX 03-SEP-1999; 99US-0389782.

XX (AMGE-) AMGEN INC.

XX Dunstan CR, Wooden SK, Mann MB;

XX WI: 2001-244572/25.
 DR Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis -
 PT
 XX Claim 3; Fig 1; 119pp; English.
 PS
 XX The patent discloses fusion protein comprising human osteoprotegerin
 CC (OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively
 CC regulates formation of osteoclasts in vitro and in vivo. It blocks
 CC the differentiation of osteoclasts from monocyte or macrophage
 CC precursors and the reabsorption of bone. The OPG-Fc fusion protein
 CC is administered for the treatment of bone loss resulting from
 CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia,
 CC osteopenia associated with surgery or steroid administration,
 CC osteonecrosis, bone loss due to rheumatoid arthritis, periodontal
 CC bone loss, osteolytic metastasis and/or prosthetic loosening.
 CC The present sequence is partial human immunoglobulin G (Ig G) 1
 CC protein comprising the hinge and heavy chain constant regions CH2
 CC and CH3.
 CC
 XX Sequence 232 AA:
 SQ
 Query Match 97.2%; Score 1225; DB 22; Length 232;
 Best Local Similarity 97.0%; Pred. No. 2.1e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSDKHTHTPCPCAPAPLLGSPVFLPPPKKOTLMISRPEVTCVAVDVSHDEPEVKF 60
 DB 1 EPKSDKHTHTPCPCAPAPLLGSPVFLPPPKKOTLMISRPEVTCVAVDVSHDEPEVKF 60
 QY 61 NMVYDGVVHNHVKTKPREEOYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
 DB 61 NMVYDGVVHNHVKTKPREEOYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEMESNGQPENNYKTTTP 180
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEMESNGQPENNYKTTTP 180
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEMESNGQPENNYKTTTP 180
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEMESNGQPENNYKTTTP 180
 QY 181 PVLDSGVSFELYSKLTVDKSRWQGNVSCSYMHALNHNHYQKSLSPGK 232
 DB 181 PVLDSGVSFELYSKLTVDKSRWQGNVSCSYMHALNHNHYQKSLSPGK 232

RESULT 4
 AAB80897
 ID AAB80897 standard; protein: 232 AA.
 XX
 AC AAB80897;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human IgGgamma1 hinge, CH2 and CH3 regions.
 XX
 XX Human; IgGgamma1; anticancer; Antimetastatic; Osteogenic;
 KW lytic bone disease; multiple myeloma; immunoglobulin;
 KW osteosclerotic bone metastasis; OPG; osteoprotegerin;
 KW osteoclast formation inhibition; bone resorption inhibition.
 XX
 OS Homo sapiens.
 XX
 PN WO200117543-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-US22806.
 XX
 PR 03-SEP-1999; 99US-0389545.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Dunstan CR;

XX WI: 2001-265936/27.
 DR Preventing or treating lytic bone diseases, particularly associated
 XX with cancer or metastasis, by administering an osteoprotegerin
 PT polypeptide -
 XX
 PS Disclosure: Fig 1; 87pp; English.
 XX
 CC The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegerin)
 CC polypeptide or OPG fusion protein. The OPG proteins (see
 CC AAB80898-AAB80905) can inhibit formation of osteoclasts (and thus bone
 CC resorption) by blocking differentiation from monocytes/macrophage
 CC precursors. The present sequence is the hinge, CH2 and CH3 regions of
 CC human IgGgamma1. This sequence can be used to generate fusion proteins of
 CC OPG and immunoglobulin, for use in the present invention. The generated
 CC fusion proteins can exhibit increased circulating half-lives and slower
 CC clearance times, thereby providing a more sustained activity.
 CC
 XX Sequence 232 AA:
 SQ
 Query Match 97.2%; Score 1225; DB 22; Length 232;
 Best Local Similarity 97.0%; Pred. No. 2.1e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSDKHTHTPCPCAPAPLLGSPVFLPPPKKOTLMISRPEVTCVAVDVSHDEPEVKF 60
 DB 1 EPKSDKHTHTPCPCAPAPLLGSPVFLPPPKKOTLMISRPEVTCVAVDVSHDEPEVKF 60
 QY 61 NMVYDGVVHNHVKTKPREEOYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
 DB 61 NMVYDGVVHNHVKTKPREEOYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEMESNGQPENNYKTTTP 180
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEMESNGQPENNYKTTTP 180
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEMESNGQPENNYKTTTP 180
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPSDIAVEMESNGQPENNYKTTTP 180
 QY 181 PVLDSGVSFELYSKLTVDKSRWQGNVSCSYMHALNHNHYQKSLSPGK 232
 DB 181 PVLDSGVSFELYSKLTVDKSRWQGNVSCSYMHALNHNHYQKSLSPGK 232

RESULT 5
 AAE15347
 ID AAE15347 standard; protein: 232 AA.
 XX
 AC AAE15347;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.
 XX
 XX Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG;
 KW cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.
 XX
 OS Homo sapiens.
 XX
 PN WO200181405-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 19-APR-2001; 2001WO-US12836.
 XX
 PR 21-APR-2000; 2000US-0559001.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Egle JC, Elliott SG, Browne JK, Sitney KC;
 DR WI: 2002-034433/04.

XX Increasing and maintaining hematocrit in mammal suffering from anemia,
 PT comprising administering hyperglycosylated analog of erythropoietin
 PT less frequently and at lower molar amount of recombinant human
 PT erythropoietin

PS Example 1; Fig 10; 95pp; English.

XX The invention relates to a method for increasing and maintaining
 CC haematocrit in a mammal. The method comprises administering a
 CC hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical
 CC composition, less frequently than an equivalent molar amount of and at
 CC a lower molar amount than recombinant human Epo (rhEpo) to obtain a
 CC comparable target haematocrit. Epo is a glycoprotein hormone necessary
 CC for the maturation of erythroid progenitor cells into erythrocytes.
 CC Human Epo analogue is useful for raising and maintaining haematocrit to
 CC a comparable target haematocrit in a mammal suffering from anaemia
 CC associated with a decline or loss of kidney function, myelosuppressive
 CC therapy comprising chemotherapeutic or anti-viral drugs or associated
 CC with excessive blood loss during surgical procedures, and in cancer
 CC condition. The present sequence is human immunoglobulin G (19g) gamma 1
 CC constant heavy chain (CH2, CH3) hinge region used to construct Epo
 CC hyperglycosylated analogue fusion protein.

SO Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 23; Length 232;

Best Local Similarity 97.0%; Pred. No. 2,1e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 1 EPKSCDTHTCPPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKF 60
 QY 61 NMVYDGEVHNVTKPREEOYNSTYRVSVLTVLHQMNMNGEKCKVSKALPAPTEKT 120
 DB 61 NMVYDGEVHNVTKPREEOYNSTYRVSVLTVLHQMNMNGEKCKVSKALPAPTEKT 120
 QY 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTP 180
 DB 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTP 180
 QY 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTP 180
 DB 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTP 180
 QY 181 PVLDSVSFFLYSKLTVDKSRMOOGNFFSCSVHMEALHNHYTKSLSPGK 232
 DB 181 PVLDSVSFFLYSKLTVDKSRMOOGNFFSCSVHMEALHNHYTKSLSPGK 232

RESULT 6

ABB09463 ID ABB09463 standard; Protein: 233 AA.

AC ABB09463;

DT 01-JUL-2002 (first entry)

DE Human IgG Fc fragment amino acid sequence.

KW Protein A; immunoglobulin G; IgG; antibody; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 168

FT Misc-difference 169 /note= "encoded by CAC"

FT Misc-difference 169 /note= "encoded by ACC"

PN WO200204602-A1.

PD 17-JAN-2002.

PF 04-JUL-2001; 2001WO-JP05788.

PR 07-JUL-2000; 2000JP-0206689.

PA (GENC-) GENCOM CORP.

PI Tanaka A, Ueda M, Teranishi Y;

DR WPI; 2002-148174/19.

DR N-PSDB; ABL52834.

PT Transformant yeast for stable supply of highly active catalytic
 PT antibody, comprises the capability of expressing and presenting protein
 PT A or its fragment, particularly with the 22 domain, on the cell surface

PS Example 3; Fig 4; 25pp; Japanese.

XX The invention relates to a transformant yeast that can present protein A
 CC or its fragment on its cell surface. The yeast can be used for detecting
 CC or isolating the Fc part of immunoglobulin (Ig)G. The yeast is useful for
 CC a stable supply of highly active catalytic antibody e.g. by screening
 CC novel functional molecules and in isolating Fc-carrying secretory
 CC proteins. The yeast of the invention is capable of adhering specifically
 CC to a combinatorial antibody library with an Fc-carrying antibody
 CC component. The current sequence represents the human IgG Fc fragment
 CC amino acid sequence.

SO Sequence 233 AA;

Query Match 97.2%; Score 1225; DB 23; Length 233;

Best Local Similarity 97.0%; Pred. No. 2,1e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 2 EPKSCDTHTCPPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKF 61
 QY 61 NMVYDGEVHNVTKPREEOYNSTYRVSVLTVLHQMNMNGEKCKVSKALPAPTEKT 120
 DB 61 NMVYDGEVHNVTKPREEOYNSTYRVSVLTVLHQMNMNGEKCKVSKALPAPTEKT 121
 QY 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTP 180
 DB 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTP 181
 QY 122 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTP 181
 DB 122 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTP 181
 QY 181 PVLDSVSFFLYSKLTVDKSRMOOGNFFSCSVHMEALHNHYTKSLSPGK 232
 DB 181 PVLDSVSFFLYSKLTVDKSRMOOGNFFSCSVHMEALHNHYTKSLSPGK 233

RESULT 7

ABB81490 ID ABB81490 standard; Protein: 251 AA.

AC ABB81490;

DT 02-SEP-2002 (first entry)

DE Human immunoglobulin gamma1 constant region protein SEQ ID NO:18.

XX Human.

XX Human: ZNF12; tumour necrosis factor receptor; cytosolic;

XX immunosuppressive; dermatological; antiinflammatory; antiadhesive;

XX neuroprotective; antirheumatic; antiarthritic; antisthmatic;

XX nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;

XX autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;

XX multiple sclerosis; insulin dependent diabetes mellitus; asthma;

XX rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;

XX glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;

XX pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;

XX light chain neuropathy; hypertension; large vessel disease;

XX graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

PN WO200238766-A2.
 XX
 XX 16-MAY-2002.
 XX
 XX
 PE 05-NOV-2001; 2001WO-US47018.
 XX
 XX 07-NOV-2000; 2000US-246449P.
 PR 20-DEC-2000; 2000US-257131P.
 PR 28-JUN-2001; 2001US-301715P.
 PR 29-AUG-2001; 2001US-315565P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gross JA, Xu W, Henne RM, Grant FJ;
 XX
 DR WPI: 2002-508212/54.
 DR N-PSDB: ABR89435.
 XX
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX
 PS Example 4; Page 143; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. Human Ztnfr12 is located to chromosome 22q13.2. The
 CC present sequence represents human immunoglobulin gamma1 constant region,
 CC which is used in an example from the present invention.
 CC
 XX
 SO Sequence 251 AA;

Query Match 97.2%; Score 1225; DB 23; Length 251;
 Best Local Similarity 97.0%; Pred. No. 2.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTPCPPAPPELLGSPVFLFPPPKKDTLMSRPEVTCVVDVSHDEPEYK 60
 DB 20 EPKSCDKHTHTPCPPAPPELLGSPVFLFPPPKKDTLMSRPEVTCVVDVSHDEPEYK 79
 QY 61 NMVYDGVENVHAKTKPREQYNSTYRVVSVLTVLIHOMMNGKREYCKKSNKALPAPIEKT 120
 DB 80 NMVYDGVENVHAKTKPREQYNSTYRVVSVLTVLIHOMMNGKREYCKKSNKALPAPIEKT 139
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTT 180
 DB 140 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTT 199
 QY 181 PVLDSVGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYQOQNSLSLSPGK 232
 DB 200 PVLDSGGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYQOQNSLSLSPGK 251

RESULT 8
 AAY24154

ID AAY24154 standard; Protein; 259 AA.
 XX
 XX AAY24154;
 AC
 XX
 DT 10-SEP-1999 (first entry)
 XX
 XX Protein from pcD51neg1 comprising human IgG1 Fc region genomic DNA.
 DE
 XX LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;
 KM low density lipoprotein; receptor; detection; immunoglobulin;
 KM fusion protein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 PN WO9932520-A1.
 XX
 PD 01-JUL-1999.
 XX
 XX 18-DEC-1998; 98WO-JP05744.
 XX
 XX 16-DEC-1998; 98JP-0358170.
 PR 19-DEC-1997; 97JP-0364981.
 PR 09-DEC-1998; 98JP-0349648.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 XX
 PI Kakutani M, Masaki T, Sawamura T;
 XX
 DR WPI: 1999-418906/35.
 DR N-PSDB: AAX88533.
 XX
 XX Fusion peptide for assay of oxidized LDL and for therapeutic use
 PT
 PS Example 1; Page 92-96; 105pp; Japanese.

XX The present invention describes a fusion peptide which consists of the
 CC extracellular domain of a mammalian oxidized LDL (low density
 CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian
 CC immunoglobulin containing all or part of the constant region. Oxidized
 CC LDL is a denatured form of LDL occurring in patients having
 CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be
 CC used for the assay of oxidized LDL in biological samples from such
 CC patients, for the diagnosis of the disorders. It can also be used
 CC therapeutically for the prevention and treatment of arteriosclerosis and
 CC hyperlipidaemia. The present sequence represents the protein from the
 CC vector DNA of pcD51neg1 comprising human IgG1 Fc region genomic DNA.
 CC
 XX
 SO Sequence 259 AA;

Query Match 97.2%; Score 1225; DB 20; Length 259;
 Best Local Similarity 97.0%; Pred. No. 2.4e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTPCPPAPPELLGSPVFLFPPPKKDTLMSRPEVTCVVDVSHDEPEYK 60
 DB 28 EPKSCDKHTHTPCPPAPPELLGSPVFLFPPPKKDTLMSRPEVTCVVDVSHDEPEYK 87
 QY 61 NMVYDGVENVHAKTKPREQYNSTYRVVSVLTVLIHOMMNGKREYCKKSNKALPAPIEKT 120
 DB 88 NMVYDGVENVHAKTKPREQYNSTYRVVSVLTVLIHOMMNGKREYCKKSNKALPAPIEKT 147
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTT 180
 DB 148 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTT 207
 QY 181 PVLDSVGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYQOQNSLSLSPGK 232
 DB 208 PVLDSGGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYQOQNSLSLSPGK 259

RESULT 9
 AAB47590

ID AAB47590 standard; Protein: 287 AA.
 AC AAB47590;
 XX
 XX 13-DEC-2001 (first entry)
 DT
 DE Fusion protein of HSA:human IgG1 Fc.
 XX
 XX Mouse; heat shock antigen; HSA: human; rat; signal transducer; CD24;
 KW fusion protein; inhibition; autoreactive T cell; atc;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
 KW systemic lupus erythematosus; psoriasis; diabetes; allergy;
 KW transplant rejection; transgenic mouse.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus musculus.
 OS
 PN WO200172325-A1.
 XX
 XX 04-OCT-2001.
 PD
 XX 29-MAR-2001; 2001WO-US40390.
 PF
 XX 29-MAR-2000; 2000US-192814P.
 PR
 XX (OHIS) UNIV OHIO STATE RES FOUND.
 XX
 PA Liu Y, Zheng P, Bai X;
 PI
 XX WPI: 2001-611581/70.
 DR N-PSDB; AAH43523, AAH43524.
 DR
 XX
 XX Inhibiting tissue destruction by autoreactive T cells, useful for
 PT treating autoimmune diseases, by administering a heat-shock
 PT antigen/CD24 polypeptide or its antibody -
 PS
 PS Disclosure; Fig 10; 34pp; English.
 PS
 CC This sequence represents a fusion protein which comprises the mouse
 CC heat shock antigen (HSA) fused to human IgG1 Fc. This protein
 CC may be used in the method of the invention for inhibiting
 CC destruction of tissue initiated by autoreactive T cells (atc). The
 CC method is especially used to treat subjects suspected of having
 CC autoimmune diseases, particularly multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, psoriasis, diabetes and
 CC allergy, also transplant rejection. Transgenic mice that express
 CC human CD24 on their T cells are useful as models for testing drugs
 CC for use against autoimmune diseases.
 CC
 SO Sequence 287 AA;
 Query Match 97.2%; Score 1225; DB 22; Length 287;
 Best Local Similarity 97.0%; Pred. No. 2.8e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 1 EPKSCDTHHCPCPAPPELLGSPVFLFPPKPKDITLMSRPEVTCVVDVSHEDPEVKF 60
 DB 56 EPKSCDTHHCPCPAPPELLGSPVFLFPPKPKDITLMSRPEVTCVVDVSHEDPEVKF 115
 OY 61 NMVYDGEVHNHAKTKPREEQYNSTYRVSVLTVLHQMNGKEYCKVSKKALPAPIEKT 120
 DB 116 NMVYDGEVHNHAKTKPREEQYNSTYRVSVLTVLHQMNGKEYCKVSKKALPAPIEKT 175
 OY 121 ISRAKVGPRPQYVYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVWESNCPENNYKTP 180
 DB 176 ISRAKVGPRPQYVYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVWESNCPENNYKTP 235
 OY 181 PVLDSVGSFLLYSKLTVDKSRMOOGNVSFSCSVHHEALHNHYOORSLSLSPGK 232
 DB 236 PVLDSVGSFLLYSKLTVDKSRMOOGNVSFSCSVHHEALHNHYOORSLSLSPGK 287
 RESULT 10

AAR91806
 ID AAR91806 standard; Protein: 329 AA.
 XX
 AC AAR91806;
 XX
 XX 20-SEP-1996 (first entry)
 DT
 DE Human immunoglobulin gamma heavy chain constant region sequences.
 XX
 XX alkaline phosphatase; label; antibody; IgG; H-chain; C-region; CH1;
 KW CH2; CH3; hinge; fusion protein; chimera; immunoassay.
 XX
 XX Homo sapiens.
 OS
 PN JP08070875-A.
 XX
 XX 19-MAR-1996.
 PD
 XX 05-SEP-1994; 94JP-0211035.
 PF
 XX 05-SEP-1994; 94JP-0211035.
 PR
 XX (TOYJ) TOSOH CORP.
 PA
 XX WPI: 1996-203155/21.
 DR N-PSDB; AAT27385.
 DR
 XX Recombinant alkaline phosphatase (AP)-antibody fusion protein -
 PT comprises AP fused downstream of antibody heavy or light chain,
 PT useful as immunoassay reagent
 PS
 PS Example 1; Page 13-15; 44pp; Japanese.
 PS
 CC The gene coding for human alkaline phosphatase is fused downstream
 CC of a gene coding for either the variable and CH1 regions of an
 CC antibody heavy chain or an antibody light chain. Coexpression of the
 CC H- and L-chain sequences, one of which is fused to the AP gene,
 CC results in production of AP-labelled antibodies suitable for use in
 CC immunoassays. The present sequence is from a human IgG heavy chain
 CC constant region.
 CC
 SO Sequence 329 AA;
 Query Match 97.2%; Score 1225; DB 17; Length 329;
 Best Local Similarity 97.0%; Pred. No. 3.2e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 1 EPKSCDTHHCPCPAPPELLGSPVFLFPPKPKDITLMSRPEVTCVVDVSHEDPEVKF 60
 DB 98 EPKSCDTHHCPCPAPPELLGSPVFLFPPKPKDITLMSRPEVTCVVDVSHEDPEVKF 157
 OY 61 NMVYDGEVHNHAKTKPREEQYNSTYRVSVLTVLHQMNGKEYCKVSKKALPAPIEKT 120
 DB 158 NMVYDGEVHNHAKTKPREEQYNSTYRVSVLTVLHQMNGKEYCKVSKKALPAPIEKT 217
 OY 121 ISRAKVGPRPQYVYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVWESNCPENNYKTP 180
 DB 218 ISRAKVGPRPQYVYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVWESNCPENNYKTP 277
 OY 181 PVLDSVGSFLLYSKLTVDKSRMOOGNVSFSCSVHHEALHNHYOORSLSLSPGK 232
 DB 278 PVLDSVGSFLLYSKLTVDKSRMOOGNVSFSCSVHHEALHNHYOORSLSLSPGK 329
 RESULT 11
 ID AAB04071 standard; Protein: 330 AA.
 AC AAB04071;
 XX
 XX 11-APR-2001 (first entry)
 DT
 XX 2cytor 10::Igg gamma fusion peptide.
 DE

XX	zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
KW	binding; detection; modulation; recombinant cell;
KW	haematopoietic cell; lymphoid cell; myeloid cell; lymph;
KW	immune system; blood; bone; inflammatory response; inflammation;
KW	spleen; human.
XX	
OS	Synthetic.
OS	Homo sapiens.
PN	WO200068381-A1.
XX	
PD	16-NOV-2000.
XX	
PF	11-MAY-2000; 2000WO-US12924.
XX	
PR	11-MAY-1999; 99US-0309861.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
PI	Presnell SR, Foster DC, Hammond AK, Lok S;
XX	
DR	WPI: 2001-016096/02.
XX	
DR	N-PSDB: AAA54473.
XX	
PT	New cytokine receptor mouse zcytor 10, useful for detecting ligands
PT	that stimulate proliferation or development of haematopoietic,
PT	lymphoid and myeloid cells
XX	
PS	Example 17; Page 120-121; 134p; English.
XX	
CC	Isolating a nucleotide which encodes the zcytor 10 cytokine
CC	receptor enables the production of recombinant cells expressing the
CC	receptor. Those cells can then be used to detect the presence of a
CC	modulator of zcytor10 protein by culturing the cells in the presence
CC	of a test ligand and comparing levels of activity of mouse zcytor10
CC	in the presence and absence of the test sample. Similarly, detection
CC	of zcytor10 receptor ligand within a test sample can be achieved.
CC	The method comprising contacting a test sample containing an amino
CC	acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC	cytokine receptor and detecting the binding of the polypeptide to a
CC	ligand in the sample. Specified peptide fragments of the zcytor 10
CC	cytokine receptor and the methods described are used to identify
CC	ligands that stimulate the proliferation and/or development of
CC	haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC	the cytokine receptor are useful for treating lymphoid, immune,
CC	inflammatory, splenic, blood or bone disorders and for generating
CC	antibodies directed against the receptor. A vector expressing a
CC	secreted human zcytor 10 heterodimer is constructed. In this
CC	construct the extracellular cytokine binding domain of zcytor 10
CC	is fused to the heavy chain of IgG gamma and the extracellular
CC	portion of the heteromeric cytokine receptor subunit (an
CC	interleukin receptor subunit) is fused to human kappa light
CC	chain (See GENSEED record AAA54474). The two sequences are fused
CC	together using two primers (AAA54475, AAA54476).
XX	
SQ	Sequence 330 AA:
Query Match	97.2%; Score 1225; DB 22; Length 330;
Best Local Similarity	97.0%; Pred. No. 3, 3e-90;
Matches 225; Conservative	3; Mismatches 4; Indels 0; Gaps 0
DB	
QY	1 EFKSCDKTHTCPRCAPFELLGSPSYFLFPFKRKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB	99 EFKSCDKTHTCPRCAPFELLGSPSYFLFPFKRKDTLMISRTPEVTCVVDVSHEDPEVKF 158
QY	61 NNYYVGVEVHNANKTRPREQYNSTYVSVLTVLHONMNMNGKPKKVSNAKALPAIIEKT 120
DB	159 NNYYVGVEVHNANKTRPREQYNSTYVSVLTVLHODWLNIGKRYKKKVSNAKALPAIIEKT 218
QY	121 ISKAYVQREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVWESNGQPENNYKTPP 180
DB	219 ISKAYVQREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVWESNGQPENNYKTPP 278

YY	181	PVLDSVSGSEFLYSKLTIVKSRMVGQGNVSCVMHEALAHNQGRSLSSGK	232
Db	279	PVLDSGSGSEFLYSKLTIVKSRMVGQGNVSCVMHEALAHNHYOKSLSSGK	330
RESULT 12			
ID	ABB81641	standard; Protein; 330 AA.	
XX	ABB81641		
AC	ABB81641		
XX	25-SEP-2002	(first entry)	
DT			
DE	Human IgG gamma 1 heavy chain SEQ ID NO:15.		
XX			
KW	Human; zcytor19; cytokine receptor; immunosuppressive; cytosolic;		
KW	antirheumatic; antiarthritic; neuroprotective; antiinflammatory;		
KW	antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;		
KW	vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;		
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;		
KW	diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;		
KW	immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;		
KW	mesangiol proliferative disease; chronic lymphocytic leukaemia; bronchitis;		
KW	secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;		
KW	haemolytic uraemic syndrome; renal neoplasia; urological neoplasia;		
KW	emphysema; chronic airway disease.		
XX			
XX	Homo sapiens.		
OS			
XX	MO200244209-A2.		
PN			
XX	06-JUN-2002.		
PD			
XX	28-NOV-2001; 2001MO-US44808.		
PF			
XX	28-NOV-2000; 2000US-253561P.		
PR	07-FEB-2001; 2001US-267211P.		
PR			
XX	(Zymo) ZYMOGENETICS INC.		
PA			
XX	Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;		
PI			
XX	WPI: 2002-527700/56.		
DR	N-PSDB: ABO73076.		
DR			
XX	Novel Zcytor19 polypeptides and polynucleotides useful for stimulating		
PT	immune responses in animals for producing antibodies, and for treating		
PT	autoimmune diseases, leukemia and asthma -		
XX			
PS	Example 7; Page 171-172; 200pp; English.		
XX			
XX	The present invention describes an isolated human zcytor19 protein (1),		
CC	and truncated zcytor19 proteins. (1) has immunosuppressive, cyostatic,		
CC	antirheumatic, antiarthritic, neuroprotective, antiinflammatory,		
CC	antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic		
CC	activities, and can be used in vaccines. (1) or an antibody binding (1)		
CC	can be used for suppressing the immune system for reducing rejection of		
CC	tissue or organ transplants and grafts and for treating T-cell specific		
CC	leukaemias or lymphomas and autoimmune diseases including rheumatoid		
CC	arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel		
CC	disease and Crohn's disease. The antibodies can also be used for treating		
CC	immunologic renal diseases, glomerulonephritis, mesangiol proliferative		
CC	disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or		
CC	vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related		
CC	diseases, amyloidosis and haemolytic uraemic syndrome. (1) and the		
CC	antibodies can also be used for renal or urological neoplasms and		
CC	multiple myelomas, asthma, bronchitis, emphysema and other chronic		
CC	airway diseases. Human zcytor19 is located to chromosome 1, more		
CC	specifically to chromosome 1p36.11. The present sequence represents		
CC	a human IgG gamma 1 heavy chain protein, which is used in an example		
CC	from the present invention.		
XX			

SQ Sequence 330 AA;
 Query Match 97.2%; Score 1225; DB 23; Length 330;
 Best Local Similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHHCPCPPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVAVVSHEDPEVKF 60
 DB 99 EPKSCDKTHHCPCPPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVAVVSHEDPEVKF 158
 QY 61 NWYDGVGVHNAVKTKPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSKALPAPLEKT 120
 DB 159 NWYDGVGVHNAVKTKPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSKALPAPLEKT 218
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 180
 DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 278
 QY 181 PVLDVSGSFLLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYQKSLSPGK 232
 DB 279 PVLDVSGSFLLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYQKSLSPGK 330

RESULT 13
 ID AAE21960; standard; Protein; 330 AA.
 AC AAE21960;
 DT 25-JUL-2002 (first entry)
 XX
 DE Human death domain containing receptor (DR6), protein-related protein.
 XX
 KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
 KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
 KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
 KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
 KW autoimmune gastritis; dermatosis; cardiopathy; infertility; haemostatic;
 KW H. pylori-associated ulceration; anti-inflammatory; vasotropic; vitreous;
 KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
 KW HIV; haemolytic uremic syndrome; HUS; immunodeficiency; neuroprotective;
 KW adult respiratory distress syndrome; ARDS; cytosolic; thyromimetic;
 KW demotological; hepatotropic; antibacterial.
 KW
 XX Homo sapiens.
 OS
 PN MO200185209-A2.
 PD 15-NOV-2001.
 XX
 PF 30-APR-2001; 2001WO-US11735.
 XX
 PR 10-MAY-2000; 2000US-203015P.
 XX
 PA (ELIL) LILLY & CO ELI.
 PI Heuer JG, Liu J, Na S, Song HY, Yang D;
 DR WPI; 2002-351283/38.
 XX
 PT Treating or preventing T cell or Th2 cell mediated condition e.g.,
 PT asthma or multiple sclerosis in mammal, comprises administering
 PT composition comprising death domain containing receptor, DR6 agonist or
 PT antagonist.
 XX
 PS Disclosure; Page 132-133; 133pp; English.
 XX
 CC The invention relates to a method for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. The
 CC method comprising administering to the mammal a pharmaceutical
 CC composition comprising a death domain containing receptor (DR6) agonist
 CC or antagonist. The method is useful for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6

CC agonist is useful in the manufacture of a medicament for treating or
 CC preventing at least one symptom associated with aberrant apoptosis,
 CC graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma,
 CC atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis,
 CC insulin-dependent diabetes mellitus, cancer, multiple sclerosis,
 CC Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic
 CC lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy,
 CC autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing
 CC lung disease, organ rejection after transplantation, thrombotic
 CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
 CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
 CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
 CC or a condition or symptom related to the above mentioned diseases in a
 CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
 CC for treating or preventing at least one symptom associated with
 CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
 CC infection, complications of infection, human immunodeficiency virus
 CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
 CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
 CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
 CC associated ulceration, cytoprotection during cancer treatment,
 CC recuperation from chemotherapy, recuperation from irradiation therapy,
 CC or a condition or symptom related to the above mentioned diseases in a
 CC mammal. The present sequence is human DR6 protein-related protein.

SQ Sequence 330 AA;
 Query Match 97.2%; Score 1225; DB 23; Length 330;
 Best Local Similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHHCPCPPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVAVVSHEDPEVKF 60
 DB 99 EPKSCDKTHHCPCPPAPPELLGSPVFLFPPKPKDTLMISRTPEVTCVAVVSHEDPEVKF 158
 QY 61 NWYDGVGVHNAVKTKPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSKALPAPLEKT 120
 DB 159 NWYDGVGVHNAVKTKPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSKALPAPLEKT 218
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 180
 DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 278
 QY 181 PVLDVSGSFLLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYQKSLSPGK 232
 DB 279 PVLDVSGSFLLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYQKSLSPGK 330

RESULT 14
 ID ABB05736
 AC ABB05736; standard; Protein; 330 AA.
 DT 01-MAY-2002 (first entry)
 XX
 DE Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
 XX
 KW Zeytor17; chromosome 5; Sg11; cytokine receptor; immunomodulatory;
 KW anti-inflammatory; antiviral; antirheumatic; antiarthritic; cytosolic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leucopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.
 KW
 XX Homo sapiens.
 OS
 PN MO200200721-A2.
 PD 03-JAN-2002.
 XX
 PR 26-JUN-2001; 2001WO-US20484.
 XX

PR 26-JUN-2000; 2000US-214282P.
 PR 29-JUN-2000; 2000US-214955P.
 PR 08-FEB-2001; 2001US-267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuljper JL;
 PI Maurer MF;
 XX
 DR WPI: 2002-090519/12.
 DR N-PSDB; ABA93797.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders -
 XX
 PS Example 17; Page 187-188; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
 CC immunity and for stimulating lymphocyte proliferation, such as in the
 CC treatment of infections involving immunosuppression, including certain
 CC viral infections. They are also useful for inducing cytotoxicity and
 CC for treating leukemias. Antagonist of zcytor17 polypeptides are useful
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention.
 CC
 XX
 SO Sequence 330 AA;
 Query Match 97.2%; Score 1225; DB 23; Length 330;
 Best Local Similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDTHTCPPAPPELLGSPVFLFPPPKRKTLMISRPETVCVVDVSHDDPEYKF 60
 DB 99 EPKSCDTHTCPPAPPELLGSPVFLFPPPKRKTLMISRPETVCVVDVSHDDPEYKF 158
 QY 61 NMVYDGEVHNHVKTKPREQYNSTYRVVSVLTVLIHOMMNGKEKCKVSNKALPAPIEKT 120
 DB 159 NMVYDGEVHNHVKTKPREQYNSTYRVVSVLTVLIHOMMNGKEKCKVSNKALPAPIEKT 218
 QY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGCPENNYKTPP 180
 DB 219 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGCPENNYKTPP 278
 QY 181 PVLDSVGSFLLYSKLTVDKSRMOGNNFSCSVMEHALHNHYQORSLSLSPGK 232
 DB 279 PVLDSGDSFLLYSKLTVDKSRMOGNNFSCSVMEHALHNHYQORSLSLSPGK 330
 RESULT 15
 ID AAM47856 standard; Protein; 330 AA.
 AC AAM47856;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 XX Human Ig-gamma1 heavy chain constant region amino acid sequence.
 DE
 XX Human Ig-gamma1 heavy chain constant region amino acid sequence.
 XX
 KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 transgenic plant.
 XX
 OS Homo sapiens.

XX
 PN WO200183529-A2.
 XX
 PD 08-NOV-2001.
 XX
 XX
 PE 28-APR-2001; 2001WO-US13932.
 XX
 PR 28-APR-2000; 2000US-200298P.
 XX
 XX
 PA (PLAN-) PLANET BIOTECHNOLOGY INC.
 XX
 PI Larrick JW, Wycoff KL;
 PI WPI: 2002-041481/05.
 DR N-PSDB; ABA05265.
 XX
 PT Immunoadhesin for treating human rhinovirus infection comprises
 PT chimeric intercellular adhesion molecule-1, and optionally a J chain
 PT and secretory component in association -
 XX
 PS Disclosure; Fig 7; 138pp; English.
 XX
 CC The invention relates to an immunoadhesin comprising:
 CC (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a
 CC rhinovirus receptor protein linked to at least a portion of an
 CC immunoglobulin heavy chain; and
 CC (b) optionally a J chain and secretory component associated with the
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
 CC glycosylation and virucide activity. The immunoadhesin is useful for
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding
 CC sites, interfering with virus entry or uncoating and directing premature
 CC release of viral RNA and formation of empty capsids. Expression of the
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.
 CC Immunoadhesin having multiple binding sites have a higher effective
 CC affinity for the virus, thereby increasing the effectiveness of the
 CC immunoadhesin. Association of secretory component and immunoglobulin J
 CC chain increases the stability of the immunoadhesin in the mucosal
 CC environment. Production is significantly less expensive in plants than in
 CC animal cell culture and production in plants is safer for human use,
 CC since plants are not known to harbor any animal viruses. The present
 CC sequence is that of a human immunoglobulin protein sequence, useful to
 CC the invention.
 CC
 XX
 SO Sequence 330 AA;
 Query Match 97.2%; Score 1225; DB 23; Length 330;
 Best Local Similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDTHTCPPAPPELLGSPVFLFPPPKRKTLMISRPETVCVVDVSHDDPEYKF 60
 DB 99 EPKSCDTHTCPPAPPELLGSPVFLFPPPKRKTLMISRPETVCVVDVSHDDPEYKF 158
 QY 61 NMVYDGEVHNHVKTKPREQYNSTYRVVSVLTVLIHOMMNGKEKCKVSNKALPAPIEKT 120
 DB 159 NMVYDGEVHNHVKTKPREQYNSTYRVVSVLTVLIHOMMNGKEKCKVSNKALPAPIEKT 218
 QY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGCPENNYKTPP 180
 DB 219 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGCPENNYKTPP 278
 QY 181 PVLDSVGSFLLYSKLTVDKSRMOGNNFSCSVMEHALHNHYQORSLSLSPGK 232
 DB 279 PVLDSGDSFLLYSKLTVDKSRMOGNNFSCSVMEHALHNHYQORSLSLSPGK 330

Search completed: July 15, 2003, 06:57:38
 Job time : 29.3185 secs

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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:59:40 ; Search time 17.7984 seconds

(without alignments)
1517.518 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260

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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1260	100.0	232	US-09-847-208-3	Sequence 3, Appl
2	1260	100.0	330	US-09-847-208-2	Sequence 2, Appl
3	1260	100.0	569	US-09-847-208-7	Sequence 7, Appl
4	1225	97.2	232	US-09-996-357-10	Sequence 10, Appl
5	1225	97.2	235	US-10-207-655-208	Sequence 208, Appl
6	1225	97.2	247	US-09-996-357-13	Sequence 13, Appl
7	1225	97.2	251	US-10-008-063-18	Sequence 18, Appl
8	1225	97.2	267	US-10-152-363A-6	Sequence 6, Appl
9	1225	97.2	288	US-09-996-357-12	Sequence 12, Appl
10	1225	97.2	288	US-09-822-851B-14	Sequence 14, Appl
11	1225	97.2	288	US-10-119-637A-14	Sequence 14, Appl
12	1225	97.2	330	US-10-047-542-20	Sequence 20, Appl
13	1225	97.2	330	US-09-995-896A-15	Sequence 15, Appl
14	1225	97.2	330	US-09-892-949-38	Sequence 38, Appl
15	1225	97.2	330	US-10-269-805-68	Sequence 68, Appl
16	1225	97.2	331	US-10-341-836-2	Sequence 2, Appl
17	1225	97.2	332	US-09-990-586-98	Sequence 98, Appl
18	1225	97.2	358	US-10-233-150-5	Sequence 5, Appl
19	1225	97.2	360	US-09-949-713-11	Sequence 11, Appl

20	1225	97.2	376	US-10-084-139-10	Sequence 10, Appl
21	1225	97.2	376	US-09-949-713-22	Sequence 22, Appl
22	1225	97.2	396	US-10-193-616-14	Sequence 14, Appl
23	1225	97.2	404	US-09-948-018-16	Sequence 16, Appl
24	1225	97.2	444	US-10-150-475A-6	Sequence 6, Appl
25	1225	97.2	447	US-09-256-156-1	Sequence 1, Appl
26	1225	97.2	451	US-10-077-033-17	Sequence 17, Appl
27	1225	97.2	451	US-09-875-338-17	Sequence 17, Appl
28	1225	97.2	451	US-09-822-698A-26	Sequence 26, Appl
29	1225	97.2	475	US-09-740-002-27	Sequence 27, Appl
30	1225	97.2	476	US-10-124-905-4	Sequence 4, Appl
31	1225	97.2	476	US-10-124-905-12	Sequence 12, Appl
32	1225	97.2	476	US-09-948-429B-4	Sequence 4, Appl
33	1225	97.2	476	US-09-948-429B-12	Sequence 12, Appl
34	1225	97.2	476	US-10-290-703-3	Sequence 3, Appl
35	1225	97.2	476	US-09-747-669-3	Sequence 3, Appl
36	1225	97.2	478	US-10-124-905-8	Sequence 8, Appl
37	1225	97.2	478	US-09-948-429B-8	Sequence 8, Appl
38	1225	97.2	480	US-10-077-023-5	Sequence 5, Appl
39	1225	97.2	480	US-10-077-023-133	Sequence 133, Appl
40	1225	97.2	480	US-10-077-023-135	Sequence 135, Appl
41	1225	97.2	480	US-09-875-338-5	Sequence 5, Appl
42	1225	97.2	492	US-10-207-655-344	Sequence 344, Appl
43	1225	97.2	499	US-10-207-655-15	Sequence 15, Appl
44	1225	97.2	499	US-10-207-655-148	Sequence 148, Appl
45	1225	97.2	500	US-10-207-655-240	Sequence 240, Appl

ALIGNMENTS

RESULT 1
US-09-847-208-3
Sequence 3, Application US/09847208
Publication No. US20030082190A1

GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daoceng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 232
TYPE: PRT
ORGANISM: Homo sapiens
US-09-847-208-3

Query Match 100.0%, Score 1260, DB 9, Length 232;
Best Local Similarity 100.0%, Pred. No. 1.6e-88;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EPKSCDKHTPCPCAPPELLGGPSVFLFPPPKKDTLMIISRPDEVTCVVDVSHEDPEYKF	60
DB	1	EPKSCDKHTPCPCAPPELLGGPSVFLFPPPKKDTLMIISRPDEVTCVVDVSHEDPEYKF	60
QY	61	NNYVDGVEVHNKTKPREBOYNSTYRVVSVLTFLHQNMMNGKEYCKVSNKALPAPIEKT	120
DB	61	NNYVDGVEVHNKTKPREBOYNSTYRVVSVLTFLHQNMMNGKEYCKVSNKALPAPIEKT	120
QY	121	ISKAVQPREPOVYTLPPSRDELITNNOVSLTLYVGFTPSDIAVENHSGQDENNYKTPP	180
DB	121	ISKAVQPREPOVYTLPPSRDELITNNOVSLTLYVGFTPSDIAVENHSGQDENNYKTPP	180
QY	181	PVLDVSGSFYLSKLTVDKSRMOQGNVFCSCVMHEALHNHYQORSLSPGK 232	
DB	181	PVLDVSGSFYLSKLTVDKSRMOQGNVFCSCVMHEALHNHYQORSLSPGK 232	

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RESULT 2
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match
Best Local Similarity 100.0%; Score 1260; DB 9; Length 330;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 99 EPKSCDTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 158
OY 61 NMVYDGEVHNKTKPREQYNSTYRVVSVLTVLIHOMNMNGEKCKVSNKALPAPIEKT 120
DB 159 NMVYDGEVHNKTKPREQYNSTYRVVSVLTVLIHOMNMNGEKCKVSNKALPAPIEKT 218
OY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPDIAVEMESNGOPENNYKTP 180
DB 219 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPDIAVEMESNGOPENNYKTP 278
OY 181 PVLDVSGSFLLYSLKLTVDKSRMOGQNFSCVMHEALHNHYQKSLSLSPGK 232
DB 279 PVLDVSGSFLLYSLKLTVDKSRMOGQNFSCVMHEALHNHYQKSLSLSPGK 330

RESULT 3
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (19G1) to CH2-CH3-CH4
; OTHER INFORMATION: (19E)
US-09-847-208-7

Query Match
Best Local Similarity 100.0%; Score 1260; DB 9; Length 569;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
OY 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
```

```
RESULT 4
US-09-996-357-10
; Sequence 10, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Getfer, Malcolm L
; APPLICANT: Isreal, David I
; APPLICANT: Joyal, John L
; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; FILE REFERENCE: PPI-105
; CURRENT APPLICATION NUMBER: US/09/996.357
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-357-10

Query Match
Best Local Similarity 97.2%; Score 1225; DB 10; Length 232;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
OY 61 NMVYDGEVHNKTKPREQYNSTYRVVSVLTVLIHOMNMNGEKCKVSNKALPAPIEKT 120
DB 61 NMVYDGEVHNKTKPREQYNSTYRVVSVLTVLIHOMNMNGEKCKVSNKALPAPIEKT 120
OY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPDIAVEMESNGOPENNYKTP 180
DB 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPDIAVEMESNGOPENNYKTP 180
OY 181 PVLDVSGSFLLYSLKLTVDKSRMOGQNFSCVMHEALHNHYQKSLSLSPGK 232
DB 181 PVLDVSGSFLLYSLKLTVDKSRMOGQNFSCVMHEALHNHYQKSLSLSPGK 232

RESULT 5
US-10-207-655-208
; Sequence 208, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207.655
```

;; CURRENT FILING DATE: 2002-07-25
;; NUMBER OF SEQ ID NOS: 426
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 208
;; LENGTH: 235
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Fusion polypeptide
US-10-207-655-208

Query Match 97.2%; Score 1225; DB 9; Length 235;
Best Local Similarity 97.0%; Pred. No. 7.6e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPGAPAPELLGSPVFLPPPKKDTLMSRPEVTCVAVDVSHEDPEVKF 60
DB 4 EPKSCDKHTHTCPGAPAPELLGSPVFLPPPKKDTLMSRPEVTCVAVDVSHEDPEVKF 63
QY 61 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 120
DB 64 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 123
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPP 180
DB 124 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPP 183
QY 181 PVLDSVGSFFLYSKLTVDKSRMWOQGVNFSCSYMHDLNHNHYQOQSLSLSPGK 232
DB 184 PVLDSGSEFFLYSKLTVDKSRMWOQGVNFSCSYMHDLNHNHYQOQSLSLSPGK 235

RESULT 6

US-09-996-357-13
;; Sequence 13, Application US/09996357
;; Patent No. US20020133001A1
;; GENERAL INFORMATION:
;; APPLICANT: Gelfer, Malcolm L
;; APPLICANT: Israel, David I
;; APPLICANT: Joyal, John L
;; APPLICANT: Gosselin, Michael
;; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
;; FILE REFERENCE: PPT-105
;; CURRENT APPLICATION NUMBER: US/09/996,357
;; PRIOR FILING DATE: 2001-11-27
;; PRIOR APPLICATION NUMBER: 60/253,302
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/250,198
;; PRIOR FILING DATE: 2000-11-29
;; PRIOR APPLICATION NUMBER: 60/257,186
;; PRIOR FILING DATE: 2000-12-20
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-996-357-13

Query Match 97.2%; Score 1225; DB 10; Length 247;
Best Local Similarity 97.0%; Pred. No. 8e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPGAPAPELLGSPVFLPPPKKDTLMSRPEVTCVAVDVSHEDPEVKF 60
DB 16 EPKSCDKHTHTCPGAPAPELLGSPVFLPPPKKDTLMSRPEVTCVAVDVSHEDPEVKF 75
QY 61 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 120
DB 76 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 135
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPP 180

DB 136 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPP 195
QY 181 PVLDSVGSFFLYSKLTVDKSRMWOQGVNFSCSYMHDLNHNHYQOQSLSLSPGK 232
DB 196 PVLDSGSEFFLYSKLTVDKSRMWOQGVNFSCSYMHDLNHNHYQOQSLSLSPGK 247

RESULT 7

US-10-008-063-18
;; Sequence 18, Application US/1008063
;; Publication No. US20030092164A1
;; GENERAL INFORMATION:
;; APPLICANT: Xu, Wenfeng
;; APPLICANT: Henne, Randal M.
;; APPLICANT: Grant, Francis J.
;; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
;; FILE REFERENCE: 00-103
;; CURRENT APPLICATION NUMBER: US/10/008,063
;; CURRENT FILING DATE: 2001-11-05
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 18
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-008-063-18

Query Match 97.2%; Score 1225; DB 9; Length 251;
Best Local Similarity 97.0%; Pred. No. 8.2e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPGAPAPELLGSPVFLPPPKKDTLMSRPEVTCVAVDVSHEDPEVKF 60
DB 20 EPKSCDKHTHTCPGAPAPELLGSPVFLPPPKKDTLMSRPEVTCVAVDVSHEDPEVKF 79
QY 61 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 120
DB 80 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 139
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPP 180
DB 140 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPP 199
QY 181 PVLDSVGSFFLYSKLTVDKSRMWOQGVNFSCSYMHDLNHNHYQOQSLSLSPGK 232
DB 200 PVLDSGSEFFLYSKLTVDKSRMWOQGVNFSCSYMHDLNHNHYQOQSLSLSPGK 251

RESULT 8

US-10-152-363A-6
;; Sequence 6, Application US/10152363A
;; Publication No. US20030103986A1
;; GENERAL INFORMATION:
;; APPLICANT: Rixon, Mark W.
;; APPLICANT: Gross, Jane A.
;; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
;; FILE REFERENCE: 01-20
;; CURRENT APPLICATION NUMBER: US/10/152,363A
;; CURRENT FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: 60/293,343
;; PRIOR FILING DATE: 2001-05-24
;; NUMBER OF SEQ ID NOS: 70
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-10-152-363A-6

Query Match 97.2%; Score 1225; DB 9; Length 251;
Best Local Similarity 97.0%; Pred. No. 8.2e-86;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
OY 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
    |||
Db 20 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 79
OY 61 NMVYDGEVHNNAKTRPREEOYNSTRYVSVLTVLHQMNMNGKEKCKVSKNALPAPIEKT 120
    |||
Db 80 NMVYDGEVHNNAKTRPREEOYNSTRYVSVLTVLHQMNMNGKEKCKVSKNALPAPIEKT 139
OY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTP 180
    |||
Db 140 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTP 199
OY 181 PVLDSGSEFLYSKLTVDKSRMGOGNVFCSCVMHEALHNNHYQKSLSLSPGK 232
    |||
Db 200 PVLDSGSEFLYSKLTVDKSRMGOGNVFCSCVMHEALHNNHYQKSLSLSPGK 251
```

RESULT 9

```
US-09-996-357-12
: Sequence 12, Application US/09996357
: Patent No. US20020133001A1
: GENERAL INFORMATION:
: APPLICANT: Gefter, Malcolm L
: APPLICANT: Isreal, David I
: APPLICANT: Joyal, John L
: APPLICANT: Gosselin, Michael
: TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
: FILE REFERENCE: PPI-105
: CURRENT APPLICATION NUMBER: US/09/996,357
: PRIOR FILING DATE: 2001-11-27
: PRIOR APPLICATION NUMBER: 60/253,302
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/250,198
: PRIOR FILING DATE: 2000-11-29
: PRIOR APPLICATION NUMBER: 60/257,186
: PRIOR FILING DATE: 2000-12-20
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 12
: LENGTH: 267
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:alpha-beta(16-30)Fc
US-09-996-357-12
```

Query Match 97.2%; Score 1225; DB 10; Length 267;
Best Local Similarity 97.0%; Pred. No. 8,8e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
OY 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
    |||
Db 36 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 95
OY 61 NMVYDGEVHNNAKTRPREEOYNSTRYVSVLTVLHQMNMNGKEKCKVSKNALPAPIEKT 120
    |||
Db 96 NMVYDGEVHNNAKTRPREEOYNSTRYVSVLTVLHQMNMNGKEKCKVSKNALPAPIEKT 155
OY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTP 180
    |||
Db 156 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTP 215
OY 181 PVLDSGSEFLYSKLTVDKSRMGOGNVFCSCVMHEALHNNHYQKSLSLSPGK 232
    |||
Db 216 PVLDSGSEFLYSKLTVDKSRMGOGNVFCSCVMHEALHNNHYQKSLSLSPGK 267
```

RESULT 10
US-09-822-851B-14
: Sequence 14, Application US/09822851B

Publication No. US20030095966A1

```
: GENERAL INFORMATION:
: APPLICANT: Liu, Yang
: APPLICANT: Zheng, Pan
: APPLICANT: Bai, Xue-Feng
: TITLE OF INVENTION: Methods of Blocking Tissue Destruction by Autoreactive T Cells
: FILE REFERENCE: 22727/04047
: CURRENT APPLICATION NUMBER: US/09/822,851B
: CURRENT FILING DATE: 2001-03-29
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 14
: LENGTH: 288
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: residues 1-52 are mouse HSA sequences, residues 53-55 are unkn
US-09-822-851B-14
```

Query Match 97.2%; Score 1225; DB 9; Length 288;
Best Local Similarity 97.0%; Pred. No. 9,6e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
OY 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
    |||
Db 56 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 115
OY 61 NMVYDGEVHNNAKTRPREEOYNSTRYVSVLTVLHQMNMNGKEKCKVSKNALPAPIEKT 120
    |||
Db 116 NMVYDGEVHNNAKTRPREEOYNSTRYVSVLTVLHQMNMNGKEKCKVSKNALPAPIEKT 175
OY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTP 180
    |||
Db 176 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTP 235
OY 181 PVLDSGSEFLYSKLTVDKSRMGOGNVFCSCVMHEALHNNHYQKSLSLSPGK 232
    |||
Db 236 PVLDSGSEFLYSKLTVDKSRMGOGNVFCSCVMHEALHNNHYQKSLSLSPGK 287
```

RESULT 11

```
US-10-119-637A-14
: Sequence 14, Application US/10119637A
: Publication No. US20030106084A1
: GENERAL INFORMATION:
: APPLICANT: Liu, Yang
: APPLICANT: Bai, Xue-Feng
: APPLICANT: Zheng, Pan
: TITLE OF INVENTION: Methods of Blocking Tissue Destruction by Autoreactive T Cells
: FILE REFERENCE: 22727/04117
: CURRENT APPLICATION NUMBER: US/10/119,637A
: CURRENT FILING DATE: 2003-02-03
: PRIOR APPLICATION NUMBER: 09/822,851
: PRIOR FILING DATE: 2001-03-29
: PRIOR APPLICATION NUMBER: 60/192,814
: PRIOR FILING DATE: 2000-03-29
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 14
: LENGTH: 288
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (1)-(52)
: OTHER INFORMATION: mouse HSA
: NAME/KEY: DOMAIN
: LOCATION: (53)-(55)
: OTHER INFORMATION: sequence created by inventor; not from any known organism
: FEATURE:
```


NAME/KEY: DOMAIN
LOCATION: (56) (288)
OTHER INFORMATION: human Ig1 Fc
US-10-119-637A-14

Query Match 97.2%; Score 1225; DB 9; Length 288;
Best Local Similarity 97.0%; Pred. No. 9.6e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPCAPPELLGPGSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 60
DB 56 EPKSCDTHTCPCPCAPPELLGPGSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 115
QY 61 NMVYDGEVHNHVKTKPREQYNSYRYVSVLTVLHONMMNGKEKCKYSNKALPAPIEKT 120
DB 116 NMVYDGEVHNHVKTKPREQYNSYRYVSVLTVLHONMMNGKEKCKYSNKALPAPIEKT 175
QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
DB 176 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 235
QY 181 PVLDSVGSFFLYSLKLTVDKSRMOQGNVFSQSVMEHALHNHYQORSLSLSPGK 232
DB 236 PVLDSGGSFFLYSLKLTVDKSRMOQGNVFSQSVMEHALHNHYQORSLSLSPGK 287

RESULT 12

US-10-047-542-20

Sequence 20, Application US/10047542
Patent No. US20020168367A1
GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.C1P1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 20
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-10-047-542-20

Query Match 97.2%; Score 1225; DB 9; Length 330;
Best Local Similarity 97.0%; Pred. No. 1.1e-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPCAPPELLGPGSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDTHTCPCPCAPPELLGPGSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 158
QY 61 NMVYDGEVHNHVKTKPREQYNSYRYVSVLTVLHONMMNGKEKCKYSNKALPAPIEKT 120
DB 159 NMVYDGEVHNHVKTKPREQYNSYRYVSVLTVLHONMMNGKEKCKYSNKALPAPIEKT 218
QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 278
QY 181 PVLDSVGSFFLYSLKLTVDKSRMOQGNVFSQSVMEHALHNHYQORSLSLSPGK 232
DB 279 PVLDSGGSFFLYSLKLTVDKSRMOQGNVFSQSVMEHALHNHYQORSLSLSPGK 330

RESULT 13

US-09-995-898A-15

Sequence 15, Application US/09995898A
Publication No. US20030027253A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Xu, Wenteng
APPLICANT: No. US20030027253A1ak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFERENCE: 00-108
CURRENT APPLICATION NUMBER: US/09/995,898A
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/267,211
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-898A-15

Query Match 97.2%; Score 1225; DB 9; Length 330;
Best Local Similarity 97.0%; Pred. No. 1.1e-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPCAPPELLGPGSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDTHTCPCPCAPPELLGPGSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 158
QY 61 NMVYDGEVHNHVKTKPREQYNSYRYVSVLTVLHONMMNGKEKCKYSNKALPAPIEKT 120
DB 159 NMVYDGEVHNHVKTKPREQYNSYRYVSVLTVLHONMMNGKEKCKYSNKALPAPIEKT 218
QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 278
QY 181 PVLDSVGSFFLYSLKLTVDKSRMOQGNVFSQSVMEHALHNHYQORSLSLSPGK 232
DB 279 PVLDSGGSFFLYSLKLTVDKSRMOQGNVFSQSVMEHALHNHYQORSLSLSPGK 330

RESULT 14

US-09-892-949-38

Sequence 38, Application US/09892949
Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuljper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-892-949-38

Query Match	97.28;	Score.1225;	DB 9;	Length 330;
Best Local Similarity	97.08;	Pred. No. 1.1e-85;		
Matches 225; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;

QY	EPKSCCKTHPCPCAPBELLGGPSVFLTPPKRKOTLMSIRPEVYCVVDYSHDPEVKF	60
Db	EPKSCCKTHPCPCAPBELLGGPSVFLTPPKRKOTLMSIRPEVYCVVDYSHDPEVKF	158
QY	NMYVDGEVHNKTKREBOYNSTYRVSVLTVLQNMNMGKEYCKSKNKALEAPLEKT	120
Db	NMYVDGEVHNKTKREBOYNSTYRVSVLTVLQNMNMGKEYCKSKNKALEAPLEKT	218
QY	ISAKAQPPPEQVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP	180
Db	ISAKAQPPPEQVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTTP	278
QY	PVLDVSGSFELYSKLTVDKSRMOQGNVFGSCVMEHALHNHQKSLSLSPGK	232
Db	PVLDVSGSFELYSKLTVDKSRMOQGNVFGSCVMEHALHNHQKSLSLSPGK	330

RESULT 15

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US-10-269-805-68
Sequence 68, Application US/10269805
Publication No. US2003012429A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-805-68

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Query Match	97.2%;	Score 1225;	DB 9;	length 330;
Best Local Similarity	97.0%;	Pred. No. 1.1e-85;		
Matches 225; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	I E P S C O K T H T C P C P A P E L I G B S F Y L R P P K D O L M T S R P E V T C V Y V D Y S H D E V K F	60
D b	99	E R K S C D K T H T C P C P A P E L I G B S F Y L R P P K D O L M T S R P E V T C V Y V D Y S H D E V K F	158
QY	61	N M Y V D G V E Y H N K T K P R E O Y N S T Y R V S Y V L T V L Q O N M N G K E Y K C K S N A L P A P I E K T	120
D b	159	N M Y V D G V E Y H N K T K P R E O Y N S T Y R V S Y V L T V L Q O D L N K E Y K C K S N A L P A P I E K T	218
QY	121	I S K A K Q P R E P O Y T L P S R D E L T K N O V S L T C L Y K G F Y P S D I A V E W E S N G O P E N N Y K T T P	180
D b	219	I S K A K Q P R E P O Y T L P S R D E L T K N O V S L T C L Y K G F Y P S D I A V E W E S N G O P E N N Y K T T P	278
QY	181	P V L D S G S F E L Y S K L T V D K S R M O G S N V S C W M H E A L H N H T Q O S L S L S G K	232
D b	279	P V L D S G S F E L Y S K L T V D K S R M O G S N V S C W M H E A L H N H T Q O S L S L S G K	330

Search completed: July 15, 2003, 07:17:18
Job time : 20.7984 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:55:24 ; Search time 9.31311 Seconds
(Without alignments)
732.958 Million cell updates/sec

Title: US-09-847-208B-3
Perfect score: 1260
Sequence: 1 EPKSCDKHTHTCPPCPAPPELL.....MHEALNHHYQORSLSPGK 232

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	232	2	US-08-595-043A-50
2	1225	97.2	331	4	US-09-178-869-2
3	1225	97.2	360	1	US-09-180-100-11
4	1225	97.2	371	1	US-08-236-311-7
5	1225	97.2	371	3	US-08-457-918-7
6	1225	97.2	376	4	US-09-180-100-22
7	1225	97.2	396	4	US-08-784-512-3
8	1225	97.2	396	4	US-09-176-228-3
9	1225	97.2	424	5	PCT-US95-03866-12
10	1225	97.2	424	5	PCT-US95-03866-14
11	1225	97.2	437	5	PCT-US96-10043-11
12	1225	97.2	442	5	PCT-US96-10043-9
13	1225	97.2	446	3	US-08-397-411-7
14	1225	97.2	449	1	US-08-458-516-13
15	1225	97.2	459	1	US-08-157-101A-7
16	1225	97.2	476	2	US-08-378-939-10
17	1225	97.2	476	3	US-08-487-550-4
18	1225	97.2	476	3	US-08-487-550-12
19	1225	97.2	478	3	US-08-487-550-8
20	1220	96.8	254	2	US-08-284-391B-33
21	1220	96.8	254	4	US-09-218-950-33
22	1219	96.7	330	4	US-09-301-593-22
23	1219	96.7	451	2	US-08-887-352B-14
24	1219	96.7	451	2	US-08-887-352B-16
25	1219	96.7	451	2	US-08-887-352B-18
26	1219	96.7	451	3	US-08-466-151-65
27	1219	96.7	451	4	US-09-109-207C-14

28	1219	96.7	451	4	US-09-109-207C-16	Sequence 16, Appl
29	1219	96.7	451	4	US-09-109-207C-18	Sequence 18, Appl
30	1219	96.7	451	4	US-09-282-505-2	Sequence 2, Appl
31	1219	96.7	451	4	US-09-054-255-2	Sequence 2, Appl
32	1219	96.7	451	4	US-09-296-005-14	Sequence 14, Appl
33	1219	96.7	451	4	US-09-296-005-16	Sequence 16, Appl
34	1219	96.7	451	4	US-09-296-005-18	Sequence 18, Appl
35	1219	96.7	452	3	US-09-027-149-71	Sequence 71, Appl
36	1219	96.7	452	4	US-09-026-985-71	Sequence 71, Appl
37	1219	96.7	452	4	US-09-121-952A-71	Sequence 71, Appl
38	1219	96.7	452	4	US-09-234-340A-71	Sequence 71, Appl
39	1219	96.7	453	3	US-08-466-151-8	Sequence 8, Appl
40	1219	96.7	453	3	US-08-466-163B-8	Sequence 8, Appl
41	1219	96.7	453	4	US-09-301-593-18	Sequence 18, Appl
42	1219	96.7	454	2	US-07-934-373C-22	Sequence 22, Appl
43	1219	96.7	454	3	US-08-437-642B-22	Sequence 22, Appl
44	1219	96.7	454	4	US-08-146-206C-22	Sequence 22, Appl
45	1219	96.7	454	5	PCT-US93-07832-22	Sequence 22, Appl

ALIGNMENTS

```
RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESSES:
ADDRESS: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-50

Query Match          97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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QY 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVK 60
DB 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVK 60
QY 61 NMVYDGVAVHNAKTKPREEOYNSTYRYVSVTLVHQNMMNGKCKYSNKAALPPIEKT 120
DB 61 NMVYDGVAVHNAKTKPREEOYNSTYRYVSVTLVHQNMMNGKCKYSNKAALPPIEKT 120

OY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP 180
121 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP 180
OY 181 PVLDSVGSFPLYSKLTVDKSRMOOGNVSFSCSVMHGALHNNHYOKSLSPGK 232
181 PVLDSGDSFPLYSKLTVDKSRMOOGNVSFSCSVMHGALHNNHYOKSLSPGK 232
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RESULT 2
US-09-178-869-2
Sequence 2, Application US/09178869B
Patent No. 6197294
GENERAL INFORMATION:
APPLICANT: Tao, Meng
APPLICANT: Wong, Shou
APPLICANT: Hickey, William F.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/178,869B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-09-178-869-2

Query Match 97.2%; Score 1225; DB 4; Length 331;
Best Local Similarity 97.0%; Pred. No. 1.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 EPKSCDKTHPCPPAPPELLGSPVFLPPPKKDTLMISRPETVCVVDVSHEDPEVKF 60
100 EPKSCDKTHPCPPAPPELLGSPVFLPPPKKDTLMISRPETVCVVDVSHEDPEVKF 159
Db 61 NMVYDGEVHNHAKTKPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSNKALPAPIEKT 120
160 NMVYDGEVHNHAKTKPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSNKALPAPIEKT 219
OY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP 180
121 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP 279
Db 220 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP 279
OY 181 PVLDSVGSFPLYSKLTVDKSRMOOGNVSFSCSVMHGALHNNHYOKSLSPGK 232
181 PVLDSGDSFPLYSKLTVDKSRMOOGNVSFSCSVMHGALHNNHYOKSLSPGK 331
Db

RESULT 3
US-09-180-100-11
Sequence 11, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-100-11

Query Match 97.2%; Score 1225; DB 4; Length 360;
Best Local Similarity 97.0%; Pred. No. 2.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 EPKSCDKTHPCPPAPPELLGSPVFLPPPKKDTLMISRPETVCVVDVSHEDPEVKF 60
129 EPKSCDKTHPCPPAPPELLGSPVFLPPPKKDTLMISRPETVCVVDVSHEDPEVKF 188
Db 61 NMVYDGEVHNHAKTKPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSNKALPAPIEKT 120
189 NMVYDGEVHNHAKTKPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSNKALPAPIEKT 248
OY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP 180
121 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP 308
Db 249 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP 308
OY 181 PVLDSVGSFPLYSKLTVDKSRMOOGNVSFSCSVMHGALHNNHYOKSLSPGK 232
181 PVLDSGDSFPLYSKLTVDKSRMOOGNVSFSCSVMHGALHNNHYOKSLSPGK 360
Db

RESULT 4

US-08-236-311-7
Sequence 7, Application US/08236311

Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adhesion Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-236-311-7

Query Match 97.2%; Score 1225; DB 1; Length 371;
 Best Local Similarity 97.0%; Pred. No. 2.2e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSRPPEVTCVAVDVSHEDPEYKF 60
 Db 140 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSRPPEVTCVAVDVSHEDPEYKF 199
 OY 61 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
 Db 200 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 259
 OY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTTT 180
 Db 260 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTTT 319
 OY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYOQRLSLSPGK 232
 Db 320 PVLDSGGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYOQRLSLSPGK 371

RESULT 5
 ; Sequence 7, Application US/08457918
 ; Patent No. 6117655

GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.

TITLE OF INVENTION: Adhesion Variants

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,918

FILING DATE: 1-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/236311

FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/936190

FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/842777

FILING DATE: 18-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/250785

FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/104329

FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:

NAME: Kubienc, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0444P1C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8228

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 371 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 US-08-457-918-7

Query Match 97.2%; Score 1225; DB 3; Length 371;
 Best Local Similarity 97.0%; Pred. No. 2.2e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSRPPEVTCVAVDVSHEDPEYKF 60
 Db 140 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSRPPEVTCVAVDVSHEDPEYKF 199
 OY 61 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
 Db 200 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 259
 OY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTTT 180
 Db 260 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTTT 319
 OY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYOQRLSLSPGK 232
 Db 320 PVLDSGGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYOQRLSLSPGK 371

RESULT 6
 ; Sequence 22, Application US/09180100
 ; Patent No. 6306395

GENERAL INFORMATION:

APPLICANT: NAKAMURA, No. 630639510

APPLICANT: NAGATA, Shigekazu

TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

FILE REFERENCE: 1110-207P

CURRENT APPLICATION NUMBER: US/09/180,100

EARLIER FILING DATE: 1998-11-02

EARLIER APPLICATION NUMBER: PCT/JP97/01502

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 22

LENGTH: 376

TYPE: PRT

ORGANISM: Homo sapiens

US-09-180-100-22

Query Match 97.2%; Score 1225; DB 4; Length 376;
 Best Local Similarity 97.0%; Pred. No. 2.2e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSRPPEVTCVAVDVSHEDPEYKF 60
 Db 145 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSRPPEVTCVAVDVSHEDPEYKF 204
 OY 61 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
 Db 205 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 264
 OY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTTT 180
 Db 265 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTTT 324
 OY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYOQRLSLSPGK 232
 Db 325 PVLDSGGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYOQRLSLSPGK 376

RESULT 7

US-08-784-512-3

; Sequence 3, Application US/08784512

; Patent No. 5872209

GENERAL INFORMATION:

APPLICANT: BARTNIK, Eckart

RESULT 8
US-09-176-228-3
: Sequence 3, Application US/09176228
: Patent No. 6180334
: GENERAL INFORMATION:
? APPLICANT: BARTNIK, Eckart
? APPLICANT: EIDENMUELLER, Bernd

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RESULT 9
PCT-US95-03866-12
; Sequence 12, Application PC/RUS9503866
; GENERAL INFORMATION:
; APPLICANT: Cytoned, Inc. (all states except US
; APPLICANT: Nocka, Karl (US only)
```

```

; APPLICANT: Lobell, Robert B (US only)
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,379
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Cytomed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-03866-12
;
; Query Match          97.2%  Score 1225; DB 5; Length 424;
; Best Local Similarity 97.0%; Pred. No. 2.7e-116;
; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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; QY 1 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSIRPEVTCVVVDVSHEDPEVKF 60
; DB 193 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSIRPEVTCVVVDVSHEDPEVKF 252
;
; QY 61 NMVYDGVGVHNAKTRPREQYNSTYRVYSVLTVFLHQNMMNGKYEYCKVSNKALPAPIEKT 120
; DB 253 NMVYDGVGVHNAKTRPREQYNSTYRVYSVLTVFLHQNMMNGKYEYCKVSNKALPAPIEKT 312
;
; QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTTTP 180
; DB 313 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTTTP 372
;
; QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYMHGALHNHYQKSLSPGK 232
; DB 373 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYMHGALHNHYQKSLSPGK 424
;
; RESULT 10
; PCT-US95-03866-14
; Sequence 14, Application PC/TUS9503866
; GENERAL INFORMATION:
; APPLICANT: Cytomed, Inc. (all states except US)
; APPLICANT: Nocke, Karl (US only)
; APPLICANT: Lobell, Robert B (US only)
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York

```

```

; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,379
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Cytomed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-03866-14
;
; Query Match          97.2%  Score 1225; DB 5; Length 424;
; Best Local Similarity 97.0%; Pred. No. 2.7e-116;
; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSIRPEVTCVVVDVSHEDPEVKF 60
; DB 193 EPKSCDKHTHTCPPCAPPELLGSPVFLPPPKKDTLMSIRPEVTCVVVDVSHEDPEVKF 252
;
; QY 61 NMVYDGVGVHNAKTRPREQYNSTYRVYSVLTVFLHQNMMNGKYEYCKVSNKALPAPIEKT 120
; DB 253 NMVYDGVGVHNAKTRPREQYNSTYRVYSVLTVFLHQNMMNGKYEYCKVSNKALPAPIEKT 312
;
; QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTTTP 180
; DB 313 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTTTP 372
;
; QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYMHGALHNHYQKSLSPGK 232
; DB 373 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSYMHGALHNHYQKSLSPGK 424
;
; RESULT 11
; PCT-US96-10043-11
; Sequence 11, Application PC/TUS9610043
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210-2804
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10043

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FILED DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-11

Query Match 97.2% Score 1225; DB 5; Length 437;
Best Local Similarity 97.0%; Pred. No. 2.8e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHHCPCPAPABELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEYKF 60
DB 206 EPKSCDTHHCPCPAPABELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEYKF 265
QY 61 NMVYDGEVHNKTKPREEOYNSTYRVSVLTVLHQMNMGKEYCKVSKALPAPIEKT 120
DB 266 NMVYDGEVHNKTKPREEOYNSTYRVSVLTVLHQMNMGKEYCKVSKALPAPIEKT 325
QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMSNQOPENNKTTTP 180
DB 326 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMSNQOPENNKTTTP 385
QY 181 PVLDSGSPFLYSKLTVDKSRMOQGNFSCSVMEALHNHYOQRSLSLSPGK 232
DB 386 PVLDSGSPFLYSKLTVDKSRMOQGNFSCSVMEALHNHYOQRSLSLSPGK 437

RESULT 12
PCT-US96-10043-9
Sequence 9, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-9

Query Match 97.2% Score 1225; DB 5; Length 442;
Best Local Similarity 97.0%; Pred. No. 2.8e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHHCPCPAPABELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEYKF 60
DB 211 EPKSCDTHHCPCPAPABELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEYKF 270
QY 61 NMVYDGEVHNKTKPREEOYNSTYRVSVLTVLHQMNMGKEYCKVSKALPAPIEKT 120
DB 271 NMVYDGEVHNKTKPREEOYNSTYRVSVLTVLHQMNMGKEYCKVSKALPAPIEKT 330
QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMSNQOPENNKTTTP 180
DB 331 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMSNQOPENNKTTTP 390
QY 181 PVLDSGSPFLYSKLTVDKSRMOQGNFSCSVMEALHNHYOQRSLSLSPGK 232
DB 391 PVLDSGSPFLYSKLTVDKSRMOQGNFSCSVMEALHNHYOQRSLSLSPGK 442

RESULT 13
US-08-397-411-7
Sequence 7, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-7

Query Match 97.2%; Score 1225; DB 3; Length 446;
Best Local Similarity 97.0%; Pred. No. 2.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSODKTHTCPPCAPPELLGGPSVFLFPPPKPTLMISRTPEVTCVAVDVSHDEPEYKF 60
DB 215 EPKSODKTHTCPPCAPPELLGGPSVFLFPPPKPTLMISRTPEVTCVAVDVSHDEPEYKF 274
QY 61 NMVYDGEVHNWKTREEOYNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 275 NMVYDGEVHNWKTREEOYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKT 334
QY 121 ISKAKVQREPOVYITLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180
DB 335 ISKAKGQREPOVYITLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 394
QY 181 PVLDSVGSFFLYSKLTVDKSRMOGNNVSCSVMEHALHNHYOQSLSLSPGK 232
DB 395 PVLDSGSEFFLYSKLTVDKSRMOGNNVSCSVMEHALHNHYOQSLSLSPGK 446

RESULT 14

US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085

GENERAL INFORMATION:

APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIb/IIIa
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 97.2%; Score 1225; DB 1; Length 449;
Best Local Similarity 97.0%; Pred. No. 2.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSODKTHTCPPCAPPELLGGPSVFLFPPPKPTLMISRTPEVTCVAVDVSHDEPEYKF 60
DB 218 EPKSODKTHTCPPCAPPELLGGPSVFLFPPPKPTLMISRTPEVTCVAVDVSHDEPEYKF 277
QY 61 NMVYDGEVHNWKTREEOYNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 278 NMVYDGEVHNWKTREEOYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKT 337
QY 121 ISKAKVQREPOVYITLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180
DB 338 ISKAKGQREPOVYITLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 397
QY 181 PVLDSVGSFFLYSKLTVDKSRMOGNNVSCSVMEHALHNHYOQSLSLSPGK 232
DB 398 PVLDSGSEFFLYSKLTVDKSRMOGNNVSCSVMEHALHNHYOQSLSLSPGK 449

RESULT 15

US-08-157-101A-7
Sequence 7, Application US/08157101A
Patent No. 5808032

GENERAL INFORMATION:

APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-BBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: TITUS, MARILANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437/204199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
TELEX: 6714627 CUCH

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-157-101A-7

Query Match 97.2%; Score 1225; DB 1; Length 459;
Best Local Similarity 97.0%; Pred. No. 3e-116;

	Matches	225;	Conservative	3;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	EPKSCDKTHTCPCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF	60							
Db	228	EPKSCDKTHTCPCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF	287							
QY	61	NWYVDGVEVHNAVKTRPREEOYNSTYRVSVLTVLHÖNMNGKEYCKKYSNKALPAPIEKT	120							
Db	288	NWYVDGVEVHNAVKTRPREEOYNSTYRVSVLTVLHODMLNGKEYCKKYSNKALPAPIEKT	347							
QY	121	ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPPSDIAVEMESNGOPENNYKTPP	180							
Db	348	ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPPSDIAVEMESNGOPENNYKTPP	407							
QY	181	PVLDSVGSFFLYSKLTYDKSRMOQGNVFSQSVMHGALHNHYOQRSLSISPGK	232							
Db	408	PVLDSVGSFFLYSKLTYDKSRMOQGNVFSQSVMHGALHNHYTKSLSISPGK	459							

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Job time : 11.3131 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:52:29 ; Search time 18.549 Seconds
(without alignments)
1657.949 Million cell updates/sec

Title: US-09-847-208b-6

Perfect score: 1/07

Sequence: 1 FTPTVKILSSCDGGGHP.....HEASPSQTVQRAVSNPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	428	1 EHHU	Ig epsilon chain C
2	1644.5	96.3	426	1 I36948	Ig epsilon chain C
3	793	46.5	429	1 EHRT	Ig epsilon chain C
4	751	44.0	388	1 EHMS	Ig epsilon chain C
5	678.5	39.7	423	1 EHMS	Ig epsilon chain C
6	576	33.7	227	1 PH215	Ig epsilon chain C
7	576	33.7	227	1 PH215	Ig epsilon chain C
8	570	33.4	115	2 E5116	Ig epsilon chain C
9	471	27.6	572	2 B46529	Ig epsilon chain C
10	471	27.6	572	2 B46529	Ig epsilon chain C
11	470	27.5	433	2 S31436	Ig epsilon chain C
12	469	27.5	504	2 S00390	Ig epsilon chain C
13	455.5	26.7	549	2 S04845	Ig epsilon chain C
14	439.5	25.7	455	1 MHMS	Ig epsilon chain C
15	439.5	25.7	455	1 MHMS	Ig epsilon chain C
16	433	25.4	328	2 A24976	Ig epsilon chain C
17	430.5	25.2	476	1 MHMS	Ig epsilon chain C
18	428.5	25.1	454	1 MHMS	Ig epsilon chain C
19	428	25.1	328	2 I47161	Ig epsilon chain C
20	416	24.4	326	1 G2HU	Ig epsilon chain C
21	415	24.3	328	2 I47159	Ig epsilon chain C
22	414	24.3	444	2 PC4436	Ig epsilon chain C
23	413.5	24.2	457	2 S03961	Ig epsilon chain C
24	413	24.2	453	2 S37768	Ig epsilon chain C
25	412	24.1	328	2 I47160	Ig epsilon chain C
26	411.5	24.1	470	2 S22080	Ig epsilon chain C
27	410	24.0	391	1 MHMS	Ig epsilon chain C
28	409.5	24.0	343	2 S25644	Ig epsilon chain C
29	409	24.0	592	2 S25705	Ig epsilon chain C

30	405.5	23.8	458	1 MHRB	Ig mu chain C regi
31	404.5	23.7	329	1 G2GP	Ig gamma-2 chain C
32	404	23.7	474	2 S15590	Ig heavy chain - h
33	402.5	23.6	452	1 MHMS	Ig mu chain C regi
34	402	23.6	324	1 G1MS	Ig gamma-1 chain C
35	400.5	23.5	277	2 I47162	Ig gamma-1 chain C
36	399	23.4	330	1 G2MSA	Ig gamma-2a chain
37	399	23.4	469	2 S37483	Ig gamma-2a chain
38	398	23.3	446	2 S40295	Ig gamma-2a chain
39	397.5	23.3	330	1 G2HU	Ig gamma-1 chain C
40	397	23.3	393	1 G1MS	Ig gamma-1 chain C
41	396.5	23.2	479	1 MHRB	Ig mu chain C regi
42	396.5	23.2	627	2 S14683	Ig mu chain precu
43	396	23.2	475	2 S01321	Ig gamma-2b chain
44	395.5	23.2	472	2 S1459	Ig gamma-1 chain
45	394	23.1	399	1 G2MSM	Ig gamma-2a chain

ALIGNMENTS

RESULT 1

EHMU
Ig epsilon chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text change 16-Jul-1999
C:Accession: A22771; A23195; PH214; A93491; A90824; A94418; B93933; S02438; A53116;
R:Flanagan, J.G.; Rabbits, T.H.
EMBO J. 1, 655-660, 1982
A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region 9
A:Reference number: A22771; MUID:84236029; PMID:6234164
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <FIA>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:q185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hatajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseu
A:Reference number: A23195; MUID:84207910; PMID:6327276
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:J00222; NID:q184755
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 2382-2392, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splic
A:Reference number: PH214; MUID:92308039; PMID:1613458
A:Accession: PH214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: EMBL:X63693; GB:S38668; NID:932987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Ono, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S
Nucleic Acids Res. 11, 719-726, 1983
A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon
A:Reference number: A93491; MUID:83168897; PMID:6300763
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:q185035
R:Max, E.E.; Batley, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945; PMID:6288268
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358, 'L', 360-428 <MAX>
A:Cross-references: GB:J00222; NID:9184755
R:Benichou, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein

A:Residues: 'GAWTL', 6, 'X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 124
 A:Experimental source: myeloma protein Nd
 R:Kerten, J.H.; Molgaard, H.V.; Houghcon, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
 A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
 A:Reference number: A93933; MUID:83065234; PMID:6815656
 A:Accession: B93933
 A:Molecule type: mRNA
 A:Residues: 1-40:68-114; 427-428 <KEN>
 A:Cross-references: GB:L00022; NID:g185035
 R:Ikemura, S.
 FEBS Lett. 224, 306-310, 1987
 A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment
 A:Reference number: S02438; MUID:86083534; PMID:3121387
 A:Accession: S02438
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 98-352 <IKE>
 R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
 J. Biol. Chem. 269, 456-462, 1994
 A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
 A:Reference number: A53116; MUID:94103254; PMID:8276835
 A:Accession: A53116
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 320-428 <ZH2>
 A:Experimental source: myeloma U266-derived cell line AF-10
 A:Note: sequence extracted from NCBI backbone (NCBI:141701, NCBIP:141702)
 R:Hellman, L.
 Eur. J. Immunol. 23, 159-167, 1993
 A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
 A:Reference number: A46536; MUID:93122085; PMID:8419166
 A:Accession: C46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 382-426 <HELD>
 A:Cross-references: GB:S55273; NID:g263166; PIDN:AMB24857.1; PID:g263167
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
 A:Accession: D46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 382-391 <HE2>
 A:Cross-references: GB:S55276; NID:g263168; PIDN:AMB24858.1; PID:g263169
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
 A:Accession: A46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 401-428 <HE3>
 A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
 C:Genetics:
 A:Gene: GDB:IGHE
 A:Cross-references: GDB:119335; OMIM:147180
 A:Map position: 14q32.33-14q32.33
 A:Introns: 1/1; 104/1; 211/1; 319/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
 F:22-87/Domain: immunoglobulin homology <IM1>
 F:128-195/Domain: immunoglobulin homology <IM2>
 F:232-301/Domain: immunoglobulin homology <IM3>
 F:338-407/Domain: immunoglobulin homology <IM4>
 F:14/Disulfide bonds: interchain (to light chain) #status predicted
 F:15-105-129-85-133-193-239-299-345-405/Disulfide bonds: #status predicted
 F:21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:121,209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 100.0%; Score 1707; DB 1; Length 428;
 Best Local Similarity 100.0%; Pred. No. 8.1e-120;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTPTPTVKILQSSCGGHHFPTIOLLCVSGTPTGTTITWLEDGQVMDVLDSTASTOE 60
 109 FTPTPTVKILQSSCGGHHFPTIOLLCVSGTPTGTTITWLEDGQVMDVLDSTASTOE 168
 QY 61 GELASTOSELTLSOKHMLSDRTTYCOVYTGHTFEDSTKCCADSNPGVSAYLSRSPFD 120
 169 GELASTOSELTLSOKHMLSDRTTYCOVYTGHTFEDSTKCCADSNPGVSAYLSRSPFD 228
 Db 121 LFIKSPITICLVVDLAPSKGTVNLTWRSRSGKRVNHNSTRKEKORNGTTLVSTLPVGT 180
 229 LFIKSPITICLVVDLAPSKGTVNLTWRSRSGKRVNHNSTRKEKORNGTTLVSTLPVGT 288
 QY 181 RDMIEGETYOCRVTHPHLPALMSTRTKTSGRAPAEVYAFATPEWPGSRDKRTLACLIQ 240
 289 RDMIEGETYOCRVTHPHLPALMSTRTKTSGRAPAEVYAFATPEWPGSRDKRTLACLIQ 348
 Db 241 NFMPEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLVETRAWEQKDEFICRAV 300
 349 NFMPEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLVETRAWEQKDEFICRAV 408
 QY 301 HEASPOTVORAVSNPGR 320
 Db 409-HEASBSQVWVORAVSNPGR 428
 RESULT 2
 136948
 Ig epsilon-chain - chimpanzee (fragment)
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 04-Oct-1996 #sequence revision 04-Oct-1996 #text-change 21-Jan-2000
 C:Accession: 136948
 R:Sakoyama, Y.; Hong, K.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
 A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang
 A:Reference number: 136948; MUID:87147196; PMID:3103123
 A:Accession: 136948
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-426 <RES>
 A:Cross-references: GB:M5398; NID:g176797; PIDN:AAA3541.6; PID:g176798
 C:Genetics:
 A:Introns: 103/1; 209/1; 317/1
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:336-405/Domain: immunoglobulin homology <IMM>
 Query Match 96.3%; Score 1644.5; DB 2; Length 426;
 Best Local Similarity 97.2%; Pred. No. 3.7e-115;
 Matches 311; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
 QY 1 FTPTPTVKILQSSCGGHHFPTIOLLCVSGTPTGTTITWLEDGQVMDVLDSTASTOE 60
 108 FTPTPTVKILQSSCGGHHFPTIOLLCVSGTPTGTTITWLEDGQVMDVLDSTASTOE 166
 Db 61 GELASTOSELTLSOKHMLSDRTTYCOVYTGHTFEDSTKCCADSNPGVSAYLSRSPFD 120
 167 GELASTOSELTLSOKHMLSDRTTYCOVYTGHTFEDSTKCCADSNPGVSAYLSRSPFD 226
 QY 121 LFIKSPITICLVVDLAPSKGTVNLTWRSRSGKRVNHNSTRKEKORNGTTLVSTLPVGT 180
 227 LFIKSPITICLVVDLAPSKGTVNLTWRSRSGKRVNHNSTRKEKORNGTTLVSTLPVGT 286
 QY 181 RDMIEGETYOCRVTHPHLPALMSTRTKTSGRAPAEVYAFATPEWPGSRDKRTLACLIQ 240
 287 RDMIEGETYOCRVTHPHLPALMSTRTKTSGRAPAEVYAFATPEWPGSRDKRTLACLIQ 346
 Db 241 NFMPEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLVETRAWEQKDEFICRAV 300
 347 NFMPEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLVETRAWEQKDEFICRAV 406
 QY 301 HEASPOTVORAVSNPGR 320
 Db 409-HEASBSQVWVORAVSNPGR 428

[illegible]

RESULT 6

Ig epsilon chain C region (version 2) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1997 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
 C:Accession: A02145
 R:Shida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.
 EMBO J. 1, 1117-1123, 1982
 A:Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with
 A:Reference number: A90966; MUID:84236092; PMID:6329728
 A:Accession: A02145
 A:Molecule type: DNA
 A:Residues: 1-423 <ISH>
 A:Note: the sequence was determined from the germline gene
 C:Genetics:
 A:Inserts: 91/1; 199/1; 307/1
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (Kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
 F:16-77/Domain: immunoglobulin homology <IMM1>
 F:115-183/Domain: immunoglobulin homology <IMM2>
 F:230-288/Domain: immunoglobulin homology <IMM3>
 F:325-396/Domain: immunoglobulin homology <IMM4>
 F:23-75,122-181,227-286,332-394/Disulfide bonds: #status predicted
 F:43,84,167,239,262,417/Binding site: carbohydrate (Asn) (covalent) #status predicted

[illegible]

```

RESULT 7
PH1215
Ig epsilon chain C region form 2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PH1215
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A:Reference number: PH1214; MUID:92308939; PMID:1613458
A:Accession: PH1215
A:Molecule type: DNA
A:Residues: 1-227 <ZHA>
A:Cross-references: EMBL:X63693
C:Genetics:
A:Introns: 108/1: 200/3
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; Immunoglobulin
F:19-88/Domain: Immunoglobulin homology <IM>

Query Match          33.7%; Score 576; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.7e-36;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      212 PRAAPEYAAFTPEWPGSRDKRTLACLIQNEPDISVQWLNHEVOLPDARHSTTPRKT 271
          |||||
Db      1 PRAPEYAAFTPEWPGSRDKRTLACLIQNEPDISVQWLNHEVOLPDARHSTTPRKT 60
          |||||

Oy      272 KGSGFEVFSRLVETRAEMEOKEFTICRAVHHAASPSQTVORAASVNG 319
          |||||
Db      61 KGSGFEVFSRLVETRAEMEOKEFTICRAVHHAASPSQTVORAASVNG 108

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RESULT 8

OY 212 PRAPEYATPWPSSRKRITACLIQNMPEDISVQLHNHVQLPDARHSTQPRKT 271
db 1 PRAPEYATPWPSSRKRITACLIQNMPEDISVQLHNHVQLPDARHSTQPRKT 60

Ig epsilon chain C region form 3 - human (fragment)
N:Alternate names: Ig epsilon chain C region, membrane-bound form (clone CH4-M2')
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text-change 21-Jan-2000
C:Accession: PH1216; D53116
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A:Reference number: PH124; MUID:92308839; PMID:1613458
A:Accession: PH1216
M:Molecule type: DNA
A:Residues: 1-243 <ZHA>
A:Cross-references: EMBL:X63693
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produced
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: D53116
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <ZH2>
A:Experimental source: myeloma U266-derived cell line AF-10
A>Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIN:141711, NCBIP:1417
C:Genetics:
A:Introns: 108/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; immunoglobulin
F:19-88/Domain: immunoglobulin homology<IMM>

Query Match 33.7%; Score 576; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 8,3e-36;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 272 KGSFVFVSRLEVTAEWEKDEFTICRAVHEAASPSQTVORAVSNPG 319
|||||
Db 61 KGSFVFVSRLEVTAEWEKDEFTICRAVHEAASPSQTVORAVSNPG 108

RESULT 9

E53116

Ig epsilon chain C region, secreted splice form (clone CH4-3'UT-CH5-M2'') - human (fragm
C:Species: Homo sapiens (man)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: E53116
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994

A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: E53116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <ZNA>

A:Experimental source: myeloma U266-derived cell line AF-10
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:19-88/Domain: immunoglobulin homology <IM>

Query Match 33.4%; Score 570; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 9,4e-36;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 212 PRAPEVYAFATPEWPGSRDKRTTACLIONFMPEDISVQWLHNEVOLDARHSTTOPRKT 271
|||||

Db 1 PRAPEVYAFATPEWPGSRDKRTTACLIONFMPEDISVQWLHNEVOLDARHSTTOPRKT 60
|||||

Oy 272 KGSFVFVSRLEVTAEWEKDEFTICRAVHEAASPSQTVORAVSNP 318
|||||

Db 61 KGSFVFVSRLEVTAEWEKDEFTICRAVHEAASPSQTVORAVSNP 107
|||||

RESULT 10

B46529

Ig y heavy chain (7.8S) - duck

N:Alternate names: Ig gamma chain (7.8S)

C:Species: Anas platyrhynchos (domestic duck)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C:Accession: B46529; S20759

R:Magor, K.E.; Watt, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992

A:Title: Structural relationship between the two Ig of the duck, Anas platyrhynchos: mc
A:Reference number: A46529; MUID:93017865; PMID:1401901
A:Accession: B46529
A:Status: preliminary
A:Molecule type: mRNA

A:Cross-references: EMBL:X65219; NID:962442; PIDN:CAA46322.1; PID:962443
A:Experimental source: spleen
A>Note: sequence extracted from NCBI backbone (NCBI:116127)

C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:37-120/Domain: immunoglobulin homology <IM>

Query Match 27.6%; Score 471; DB 2; Length 572;
Best Local Similarity 32.0%; Pred. No. 1.6e-27;

Matches 106; Conservative 66; Mismatches 141; Indels 18; Gaps 10;

Oy 2 TPPIYKIIQSS-CDGGHFPPTIQLCLVSGTPTGNTITWLEDQVMDVLDASTAOE 60
|||||

Db 248 TPPEVOVLHSSVCSLIG--DDSVELLCVITGFSPPVEVWLVDG--APAHLVATMPPO 303
|||||

Oy 61 GELAS----TQSELTLSQKHWLSDRTYCOVTV--OGTFPESTKCKADSNPRG---VSA 111
|||||

Db 304 REAGSKTMTATSOQVNSHEDKAKGAFCTCRVKAHPATGTGAOCHAFCGSGAQSSPIQI 363
|||||

Oy 112 YLSRSPDPLFIRKSPITTCVLVDLAPSKGTVNLTWASRASKPVNHNSTRKEKORNGTLT 171
|||||

Db 364 FVPPSPSCLYTRDPAKHVCLVNL--PEDASTLSISWTRREKSGALRPDPMVLTEHNGFT 422
::: |||

Oy 172 VTSFLPVGTRWIGETVQCRTVHPHLPALMRSTTKSGRAPEVYAFATPEWPGSRD 231
::: |||

Db 423 ASSSLAISTQDMLGERFTCTVQHEDLPVPLGKSLAKHAGVTAAPYTFPPHAEELSLA 482
::: |||

Oy 232 KRTIACLIONFMPEDISVQWLHNEVOLDARHSTTOP-RKTKSGS-FFVFSRLEVTAEW 289
::: |||

Db 483 EYTLTCLVRGFOPEVEVQWLRNHNNSVALEFVITPLPKRNGDSTFFLYSKMTVPKASW 542
::: |||

Oy 290 EQKDEFTICRAVHEAASPSQTVORAVSNPG 320
::: |||

Db 543 QGVSVACMVVHEGL-PMRFQRPRLQKTPGK 572
::: |||

RESULT 11

S31436

Ig upsilon chain - axolotl (fragment)

C:Species: Ambystoma mexicanum (axolotl)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999

C:Accession: S31436
R:Fellah, J.S.; Wiles, M.V.; Schwager, J.; Charlemagne, J.

submitted to the EMBL Data Library, November 1992

A:Description: cDNA sequence of Ambystoma mexicanum upsilon heavy Ig chain.

A:Reference number: S31436
A:Accession: S31436
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-433 <FEEL>

A:Cross-references: EMBL:X69492; NID:962421
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 27.5%; Score 470; DB 2; Length 433;
Best Local Similarity 31.0%; Pred. No. 1.3e-27;

Matches 102; Conservative 72; Mismatches 137; Indels 18; Gaps 9;

Oy 4 PTVKIIQSSC--DGGHFPPTIQLCLVSGTPTGNTITWLEDQVMDVLDASTAOE 60
::: |||

Db 111 PSYQVLOSSCADTDSNG-----SIELVCLISGTPTNIGVRLVNDKMAPFIOGQTSPPKQD 166
::: |||

Oy 61 GE-LASTQSELTLSQKHWLSDRTYCOVTVGHT--FEDSTRKCKADS-NPRGVSAYLSRP 116
::: |||

Db 167 GGGTFSTTSQINVTWKSDWASDCKYCKEHPATSSRAEDTTHNCADSOPTPOPKVFLIAP 226
::: |||

Oy 117 SPFDLFIKSPITTCVLVDLAPSKGTVNLTWASRASKPVNHNSTRKEKORNGTLT 176
::: |||

Db 227 KARDLYIANOPVILCKITRKMS--DLSLVTKRRRGPREAAVISQYIDSGFTFAMSYL 285
::: |||

Oy 177 PVGTRDWIEGETVQCRTVHPHLPALMRSTTKSGRAPEVYAFATPEWPGSRDKRTL 235
::: |||

Db 286 NITKNEWRGDEFTCKVHHPDLRPLSLSVSKSPTRSRAPNYVAHPHEMLANTDPSL 345
::: |||

Oy 236 ACLIONFMPEDISVQWLHNEVOLDARHSTTOPRKTGSG---FFVFSRLEVTAEWEQ 291
::: |||

Db 346 TCLVKSFSPPDDIYIOWKQGSVIPSCKVSMPEPROEAGTAGTGYFSYMLTIQSDWK 405
::: |||

Oy 292 KDEFTICRAVHEAASPSQTVORAVSNPG 320
::: |||

Db 406 RETFTCVAAHSAV-PKNLMTTRIRQPLGK 433
::: |||

RESULT 12

S00390

Ig gamma chain (clone 36) - chicken (fragment)

N:Alternate names: Ig nu chain

C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000

C:Accession: S00390
R:Parvart, R.; Avivi, A.; Leshner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter,
EMBO J. 7, 739-744, 1988

A:Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combi
A:Reference number: S00390; MUID:88283642; PMID:3135182

A:Accession: S00390
 A:Molecule type: mRNA
 A:Residues: 1-504 <PAC>
 A:Cross-references: EMBL:X07174
 A:Note: this sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 27.5%, Score 469, DB 2; Length 504;
 Best Local Similarity 32.4%, Pred. No. 1.9e-27;
 Matches 108; Conservative 60; Mismatches 143; Indels 22; Gaps 9;

4 PTYKILQ--SCDGGGHPPTIOLCLVSGYPTGNTINWLEGGVMDVLTASTQGE 62
 178 PEVYLHRASSCTPSP--SEVELLCLVTGFSPPASAEVWLVGGGLVVASQSPAVRSGS 235
 63 LASTOSELLTSOKHMLSDRYTCQVY--QGHFFEDSTKRCADS---NPRGVSATLSRP 116
 236 TYSLSRNVNCGTDMREKSKYSCHVRHPATNTVVEDHVGCPDQAGSCP--IQLYALPP 293
 117 SPDLFLRKSPITICLVVDLAPSKGVNVLWVSRAKGFVNHSRKREKQKNGTLTVSTL 176
 294 SPGLLYISLDAKLCLVYNL-PSDSLSLVTWTRKSGNLRPDPVWLOEHFNGTYSASGAV 352
 177 PVGRDMIEGTYOCRTVHPHLPALMSTKTSGRNAPRVYAFATPEMGSRDKRTLA 236
 353 PVSTQDMISGRFTCTVOHEELPLPLSKSVYKNTGPTTPPLYPAPHPHEELSLSRVTL 412
 237 CLIONFPEDISVOMLHNEVOLPDARHSTT---QPRKTKSGS-----FEVFSLEVT 287
 413 CLVGFPRPRDIEIRMLRHRVAPATEFVYTAVLPREERANAGGDDFFFYKMSVETA 472
 288 EMEQKDEFICAVHEASPSQTVORANVSVPNGK 320
 473 KMGNGTVFACAVHVAL-PMRFSORTLQKQAK 504

RESULT 13

19 heavy chain precursor - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
 C:Accession: S04845; S05695
 R:Amemiya, C.T.; Haire, R.N.; Litman, G.W.
 A:Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin
 A:Reference number: S04845; MUID:89345103; PMID:2503814
 A:Accession: S04845
 A:Molecule type: mRNA
 A:Residues: 1-549 <AME>
 A:Cross-references: EMBL:X15114
 R:Litman, G.W.
 Submitted to the EMBL Data Library, April 1989
 A:Reference number: S05695
 A:Accession: S05695
 A:Molecule type: mRNA
 A:Residues: 1-3308, 'H', 310-549 <LIT>
 A:Cross-references: EMBL:X15114; NID:964799; PID:9763031
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin
 F:26-109/Domain: immunoglobulin homology <IMM>
 F:281,294/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 26.7%, Score 455.5; DB 2; Length 549;
 Matches 106; Conservative 60; Mismatches 140; Indels 15; Gaps 8;

4 PTYKILQSCDGGGHPPTIOLCLVSGYPTGNTINWLEGGVMDVLTASTQGE 62
 240 PVEILLQPCASS---KVELLCLVTGFSPPASAEVWLVGGGLVVASQSPCKCKENG 295
 63 LASTOSELLTSOKHMLSDRYTCQVY--QGHFFEDSTKRCADS--NPRGVSATLSRSPFD 120

296 TFSRSKVSVPKEDMNSDSTCKVTHPASHTKTEASTKCC-DETAITPKVVDLPPSPKD 354
 121 LPIKSPITICLVVDLAPSKGVNVLWVSRAKGFVNHSRKREKQKNGTLTVSTLPVGT 180
 355 LLYTRKAVYCVISMMA-STDDLYQWRSRSGKALADSAPEKAYDFTFYKSTLTKSP 413
 181 RDWIEGEFYQCRVTHPHLPALMSTKTSGRNAPRVYAFATPEMGSRDKRTLA 240
 414 GDWENKQFNCVKVHPDLPSPTEKSKODPGTEPTTLPPSDDELNDPISLICMLK 473
 241 NEMPEDISVOMLHNEVOLPDARHSTTP-RRTKSGSFPVFSRLVETRAEMQKDEFCORA 299
 474 NFRPDIVYFKKGVVLTEDYMTTTPVLEEBEGFISFKLTARSDDMMKATYSCTA 533
 300 VHEASPSQTVORANVSVPNGK 320
 534 AHNTIS-----QROIKNRKG 549

RESULT 14

MMS

19 mu chain C region, secreted form - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 16-Aug-1996
 C:Accession: A02166; A26239; A26240; B02039
 R:Kawakami, T.; Takahashi, N.; Honjo, T.
 A:Title: Complete nucleotide sequence of mouse immunoglobulin mu gene and comparison
 A:Reference number: A02166; MUID:81076590; PMID:6255422
 A:Accession: A02166
 A:Molecule type: DNA
 A:Residues: 1-455 <KAW>
 A:Cross-references: GB:J00443
 A:Note: the sequence was determined from the germline gene
 R:Goldberg, G.I.; Vanin, E.F.; Zrolka, A.M.; Blattner, F.R.
 Gene 15, 33-42, 1981
 A:Title: Sequence of the gene for the constant region of the mu chain of Balb/c mouse
 A:Reference number: A26239; MUID:82051295; PMID:6795090
 A:Accession: A26239
 A:Molecule type: DNA
 A:Residues: 1-455 <GOL>
 A:Note: the sequence was determined from the germline gene
 R:Auffray, C.; Rougeon, F.
 Gene 12, 77-86, 1980
 A:Title: Nucleotide sequence of a cloned cDNA corresponding to secreted mu chain of m
 A:Reference number: A26240; MUID:81165562; PMID:6260591
 A:Contents: TEPC183
 A:Accession: A26240
 A:Molecule type: mRNA
 A:Residues: 1-225, 'N', 227-257, 'S', 259-367, 'K', 369-455 <AUF>
 R:Keniry, M.; Sibley, C.; Fuhrman, J.; Schilling, J.; Hood, L.E.
 Proc. Natl. Acad. Sci. U.S.A. 76, 2932-2936, 1979
 A:Reference number: A26241; MUID:79223904; PMID:111247
 A:Contents: annotation: MOPC 104E
 A:Note: this sequence has been revised in reference A02039. Carbohydrate binding site
 R:Keniry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
 Biochemistry 21, 5415-5424, 1982
 A:Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain
 A:Reference number: A02039; MUID:83075344; PMID:6816276
 A:Contents: MOPC 104E
 A:Accession: B02039
 A:Molecule type: Protein
 A:Residues: 1-77, 'N', 79-100, 'Q', 102-225, 'N', 227-257, 'T', 259-367, 'K', 369-455 <KEH>
 C:Genetics:
 A:Insertions: 1/1; 106/1; 219/1; 325/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl
 F:21-91/Domain: immunoglobulin homology <IMM1>
 F:129-201/Domain: immunoglobulin homology <IMM2>
 F:239-307/Domain: immunoglobulin homology <IMM3>
 F:346-417/Domain: immunoglobulin homology <IMM4>

F:436->Domain: carbonyl-terminal <CTS> #status predicted
 E:146/Disulfide bonds: interchain (to light chain) #status predicted
 F:28-89/Disulfide bonds: #status experimental
 F:446-211,243-281,442/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:136-159,246-305,353-415/Disulfide bonds: #status predicted
 F:1293/Disulfide bonds: interchain (to heavy chain) #status predicted
 F:1293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match	25.7%;	Score 439.5;	DB 1;	Length 455;
Best Local Similarity	32.3%;	Pred. No. 2.7e-25;		
Matches 106; Conservative	57;	Mismatches 152;	Indels 13;	Gaps 8;

OY	4	PTVKLJSSCDD-GGHEPPTJDLVLVSZTGTJINVLJEGOVADVLSSTQEGE	62
Db	112	PVNANFVPRDGFSSPAPRKSLICEATNFTRKPIVLVSLKMGKLVESGFTTDPVATENK	171
OY	63	LASTO-----SELLTSOKHMLSDRITYTCOYVYQGHTF-EDSTKCADSNRGVATLSRP	116
Db	172	GSTPDQYKVISLTLTSEIDMLNLANYTCVCDHRGTFELNVNSTCASAASSTDLTFPTIP	231
OY	117	SPFDLFIRKSPITLTCLVUDLAPSKGTVNLTWASRAGRPVNHSHRKEEKNRGTLVYSTL	176
Db	232	SPADIFLEKSANLTLVLVSLMAYTE-PLNLSMASQSEPERLETKIKIMESHNGFFSAKGYA	290
OY	177	PYGTDMJEGEYTCQRVTHPHPLRALMBSITTSQGRAPAEVYATFP--EWFSGSDKRT	234
Db	291	SVCVEEDMNNRKEFVCTVYTHRDLPSPOKRTISKRNEYHNKHPRAYLLPRAEQOINLESAT	350
OY	235	LACTIIONMPEDISVOWMLNEVOLDPARHSTTOPRKTGKS-GF-FVFSRLYVRAEMEQ	292
Db	351	VTCLVKGFSPADISVOWLORGLLPQEKAVTSAHPMEPCGAPGYLFTHSLITVTEEBMNSG	410
OY	293	DEFICRAVHEAASPSQOYORAVSVNFGK	320
Db	411	ETVTCVVGHEAL-PHLVTERIVDKSTGK	437

RESULT 15

A24976
 Ig mu chain C region (allele b) - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
 C.Accession: A24976
 R.Schreier, P.H., Quester, S.; Bothwell, A.
 Nucleic Acids Res. 14, 2381-2389, 1986
 A.Title: Allotypic differences in murine mu-genes.
 A.Reference number: A24976; MID:8616735; PMID:3083402
 A.Accession: A24976
 A.Molecule type: mRNA
 A.Residues: 1-455 <SCCH>
 A.Cross-references: GB:003690; NID:952381; PIDN:CAA27326.1; PID:952382
 A.Experimental source: strain C57BL/6
 A.Note: the authors translated the codon AAG for residue 65 as Leu
 C.Superfamily: Immunoglobulin C region; immunoglobulin homology
 E:346-417/Domain: immunoglobulin homology <IMM>

Query Match	25.7%;	Score 439.5;	DB 2;	Length 455;
Best Local Similarity	32.3%;	Pred. No. 2.7e-25;		
Matches 106;	Conservative 57;	Mismatches 152;	Indels 13;	Gaps 8

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:47:19 ; Search time 9.99108 Seconds
(without alignments)
1328.428 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVRIKILSSCDGGHFP.....HEASPSQTVGRVSNPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1707	100.0	428	1 EPC_HUMAN	P01854 homo sapien
2	793	46.5	429	1 EPC_RAT	P01855 rattus norv
3	751	44.0	421	1 EPC_MOUSE	P06336 mus musculu
4	439.5	25.7	455	1 MUC_MOUSE	P01872 mus musculu
5	430.5	25.2	476	1 MUCM_MOUSE	P01873 mus musculu
6	423.5	24.8	454	1 MUC_MESAU	P06337 mesocricetu
7	416	24.4	326	1 GC2_HUMAN	P01859 homo sapien
8	413.5	24.2	457	1 MUC_SUNMU	P20768 stuncus muli
9	410	24.0	391	1 MUCB_HUMAN	P04220 homo sapien
10	405.5	23.8	454	1 MUC_HUMAN	P01871 homo sapien
11	405.5	23.8	458	1 MUC_RABIT	P03988 coryctolaqus
12	404.5	23.7	329	1 GC2_CAVPO	P01862 cavia porce
13	402	23.6	324	1 GC1_MOUSE	P01868 mus musculu
14	399	23.4	330	1 GCMA_MOUSE	P01863 mus musculu
15	397.5	23.3	330	1 GC1_HUMAN	P01857 homo sapien
16	397	23.3	393	1 GC1M_MOUSE	P01869 mus musculu
17	396.5	23.2	479	1 MUCM_RABIT	P04221 coryctolaqus
18	394	23.1	399	1 GCAM_MOUSE	P01865 mus musculu
19	390	22.8	336	1 GCB_MOUSE	P01866 mus musculu
20	389	22.8	450	1 MOC_CANFA	P01874 canis famli
21	386.5	22.6	323	1 GC_RABIT	P01870 coryctolaqus
22	386.5	22.6	329	1 GGC_RAT	P20762 rattus norv
23	385.5	22.6	327	1 GC4_HUMAN	P01861 homo sapien
24	385.5	22.6	333	1 GCB_RAT	P20761 rattus norv
25	385	22.6	405	1 GCBM_MOUSE	P01867 mus musculu
26	377	22.1	329	1 GC3_MOUSE	P22436 mus musculu
27	376	22.0	322	1 GCA_RAT	P20760 rattus norv
28	369	21.6	326	1 GC1_RAT	P20759 rattus norv
29	366	21.4	398	1 GC3M_MOUSE	P03987 mus musculu
30	362.5	21.2	335	1 GCAB_MOUSE	P01864 mus musculu
31	347	20.3	340	1 ALC2_HUMAN	P01877 homo sapien
32	345.5	20.2	290	1 GC1_HUMAN	P01860 homo sapien
33	334.5	19.6	353	1 ALC1_HUMAN	P01876 homo sapien

34	327	19.2	438	1 HVCS_HETFR	P23087 heterodontu
35	326	19.1	353	1 ALC1_GORGO	P20758 gorilla gor
36	324	19.0	438	1 HVCS_HETFR	P23085 heterodontu
37	321	18.8	393	1 HVCS_HETFR	P23086 heterodontu
38	318	18.6	461	1 HVCM_HETFR	P23087 heterodontu
39	310	18.2	446	1 MOC_CHICK	P01875 gallus gall
40	304	17.8	370	1 HVCI_HETFR	P23084 heterodontu
41	303	17.8	344	1 ALC_MOUSE	P01878 mus musculu
42	236.5	13.9	299	1 ALC_RABIT	P01879 coryctolaqus
43	228.5	13.4	481	1 MUCM_ICTPU	P23735 icetalurus p
44	193	11.3	383	1 DTC_HUMAN	P01880 homo sapien
45	148	8.7	104	1 LAC2_RAT	P20767 rattus norv

ALIGNMENTS

RESULT 1	ID	Sequence	STANDARD	PRT	428 AA.
AC	P01854:				
DT	21-JUL-1986 (rel. 01, Created)				
DT	21-JUL-1986 (rel. 01, Last sequence update)				
DT	15-JUN-2002 (rel. 41, Last annotation update)				
DE	Ig epsilon chain C region.				
GN	IGH.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83168897; PubMed=6300763;				
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,				
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;				
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin				
RT	epsilon chain cDNA."				
RL	Nucleic Acids Res. 11:719-726(1983).				
RN	[2]				
RP	SEQUENCE FROM N.A., AND VARIANT LEU-359.				
RX	MEDLINE=83001945; PubMed=6288268;				
RA	Max E.E., Batley J., Ney R., Kirsch I.R., Leder P.;				
RT	"The sequence of a human immunoglobulin epsilon chain constant				
RT	region gene, and evidence for three non-allelic genes."				
RL	EMBO J. 1:655-660(1982).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84236029; PubMed=6234164;				
RA	Flanagan J.G., Rabbits T.H.;				
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant				
RT	region gene, and evidence for three non-allelic genes."				
RL	EMBO J. 1:655-660(1982).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84207910; PubMed=6327276;				
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;				
RT	"Long terminal repeat-like elements flank a human immunoglobulin				
RT	epsilon pseudogene that lacks introns."				
RL	EMBO J. 1:1539-1544(1982).				
RN	[5]				
RP	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).				
RA	Benich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;				
RT	(In) Bach M.K. (eds.);				
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,				
RL	Marcel Dekker, New York (1978).				
RN	[6]				
RP	SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.				
RX	MEDLINE=83065234; PubMed=6815656;				
RA	Kenlen J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,				
RA	Bell L.O., Gould H.J.;				
RT	"Cloning and sequence determination of the gene for the human				
RT	immunoglobulin epsilon chain expressed in a myeloma cell line."				
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).				
RN	[7]				


```

QY 121 LFIKSPITCLVVDLPASRGTVNLWTSRSGKPVNHSSTREKORNGTLVSTLPVGT 180
D 220 LVENGTFKRLICLVLDL-ESEENITVTVWRERKKSIGASQSTKHNNATISITSLPVDA 278
QY 181 KDWIEGTQYOCRVTHPHLPALMRSTKTSQPPRAPEVYAFAPPEWPGSRDKRTLACLIQ 240
D 279 KDWIEGTQYOCRVTHPHLPALMRSTKTSQPPRAPEVYAFAPPEWPGSRDKRTLACLIQ 337
QY 241 NFMEDISVQMLNHEVOLPDARHSTQPRKTKSG--FFVRSRLVETRAEMEQDEFICR 298
D 338 NFMEDISVQMLNHEVOLPDARHSTQPRKTKSG--FFVRSRLVETRAEMEQDEFICR 397
QY 299 AVHEASPSQTVQRAVSVPNG 319
D 398 VIHEALPKRKLERTIKSLG 418

RESULT 3
EPC_MOUSE STANDARD; PRT; 421 AA.
ID EPC_MOUSE STANDARD; PRT; 421 AA.
AC P06336; P01856; (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig epsilon chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP MEDLINE-84236092; PubMed-6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RL comparison with the human epsilon gene sequence.";
EMBL J. 1:1117-1123(1982).
RN [2]
RP REVISIONS.
RA Honjo T.;
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
RN [3]
RP MEDLINE-8311774; PubMed-6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
RL chain cDNA.";
PUB. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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CC -----
DR EMBL: X01857; CAA25977.1; -
DR EMBL: X01857; CAA25978.1; -
DR PIR: A02145; EHMS.
DR PIR: A02145; EHMS.
DR HSSP: P01854; IIG.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cI.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00410; Ig_Like; 2.
DR SMART: SM00407; IGc1; 2.
DR PROSITE: PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.

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FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 BY SIMILARITY.
FT DISULFID 121 180 BY SIMILARITY.
FT DISULFID 226 285 BY SIMILARITY.
FT DISULFID 330 392 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 421 AA; 47320 MW; 8F909E130A06B47 CRC64;

Query Match 44.0%; Score 751; DB 1; Length 421;
Best Local Similarity 45.8%; Pred. No. 7.5e-53;
Matches 147; Conservative 59; Mismatches 109; Indels 6; Gaps 5;

QY 2 TPPTVKLQSSCGGHPPTIOLCLVSGTPTGNTIWL-EDGYMDVDLSTASTOE 60
D 97 TEPTLELHSSCDPNA-FHSTIQLYCEYGIHLNDVSVWLMDDREITDPLAQTVLAKKE 155
QY 61 GELASTQSELTLISQKHWLSDRTYQCVYQGFEDSTTKKCADSNPRGVSATLSRPSF 120
D 156 GKLASTQSKLNTITQOMMSEETFTCKYTSQGVLDLHTRCRDHPERGVTIYLLRPSPLD 215
QY 121 LFIKSPITCLVVDLPASRGTVNLWTSRSGKPVNHSSTREKORNGTLVSTLPVGT 180
D 216 LYONGAPKRLICLVLDLSEK-NVNVTNQOEKTSVASQWYTKHNNATISITSLPVDA 274
QY 181 KDWIEGTQYOCRVTHPHLPALMRSTKTSQPPRAPEVYAFAPPEWPGSRDKRTLACLIQ 240
D 275 KDWIEGTQYOCRVTHPHLPALMRSTKTSQPPRAPEVYAFAPPEWPGSRDKRTLACLIQ 333
QY 241 NFMEDISVQMLNHEVOLPDARHSTQPRKTKSG--FFVRSRLVETRAEMEQDEFICR 298
D 334 NFMEDISVQMLNHEVOLPDARHSTQPRKTKSG--FFVRSRLVETRAEMEQDEFICR 397
QY 299 AVHEASPSQTVQRAVSVPNG 319
D 394 VIHEALPKRKLERTIKSLG 414

RESULT 4
MOC_MOUSE STANDARD; PRT; 455 AA.
ID MOC_MOUSE STANDARD; PRT; 455 AA.
AC P01872;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig mu chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP MEDLINE-81076590; PubMed-6255422;
RA Kawakami T., Takahashi N., Honjo T.;
RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and
RL Nucleic Acids Res. 8:3933-3945(1980).
RN [2]
RP MEDLINE-82051295; PubMed-6795090;
RA Goldberg G.I., Vanin E.F., Zrolka A.M., Blattner F.R.;
RT "Sequence of the gene for the constant region of the mu chain of
RL Balb/c mouse immunoglobulin.";
Gene 15:33-42(1981).
RN [3]

```

SEQUENCE FROM N.A. (MYELOMA TERC183).
 RA MEDLINE-81165562; PubMed-6260591;
 RA Aulfray C., Rougeon F.;
 RT "Nucleotide sequence of a cloned cDNA corresponding to secreted mu
 chain of mouse immunoglobulin.";
 RL Gene 12:77-86(1980).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
 RX MEDLINE-7923904; PubMed-111247;
 RA Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood L.E.;
 RT "Amino acid sequence of a mouse immunoglobulin mu chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
 RN [5]
 RP REVISION (MOPC 104E).
 RX MEDLINE-83075344; PubMed-6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 heavy chain constant region domains.";
 RL Biochemistry 21:5415-5424(1982).
 CC -1- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
 SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
 CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
 TERMINAL SEGMENTS.
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 DR EMBL; V00827; -; NOT_ANNOTATED_CDS.
 DR PIR; A02167; MHMS.
 DR HSSP; P01857; 1FC1.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003597; Iq-cl.
 DR InterPro; IPR003600; Iq_1like.
 DR Pfam; PF00047; Iq; 4.
 DR SMART; SM00410; Iq_1like; 2.
 DR SMART; SM00407; Igcl; 2.
 DR PSORT; PS00290; Iq_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1
 FT DOMAIN 1 105
 FT DOMAIN 106 217
 FT DOMAIN 218 324
 FT DOMAIN 325 436
 FT DOMAIN 437 455
 FT DISULFID 14
 FT DISULFID 28 89
 FT DISULFID 136 199
 FT DISULFID 216 305
 FT DISULFID 246 305
 FT DISULFID 293 293
 FT DISULFID 353 415
 FT DISULFID 454 454
 FT CARBOHYD 46 46
 FT CARBOHYD 243 243
 FT CARBOHYD 281 281
 FT CARBOHYD 442 442
 FT VARIANT 78 78
 FT VARIANT 101 101
 FT VARIANT 226 226
 FT VARIANT 258 258
 FT VARIANT 258 258
 FT VARIANT 368 368
 SQ SEQUENCE 455 AA; 50101 MW; 4CB57CB602F9B51 CRC64;
 Query Match 25.7%; Score 439.5; DB 1; Length 455;

Best Local Similarity 32.38; Pred. No. 6,7e-28;
 Matches 106; Conservative 57; Mismatches 152; Indels 13; Gaps 8;
 QY 4 PTVKIIQSSCDG-GGHPPTIOLLCLIVSGYTPGINTIWMLEGGVMDLSTSTQEGE 62
 Db 112 PNVNVPFPPRDGFGSPAPRKSRLKICENTNTPKITYSWLKDGVLVSGFTTDPVTE 171
 QY 63 LASTQ-----SELTLSQKHWLSDRTYCYQVYGGHFE-EDSTKCKADSNRGVAYLSRP 116
 Db 172 GSPOTVKVISTLILSEIDMLNVLNVCYCRVDHRELFLKNNVSTPCASPSDILFTIPP 231
 QY 117 SPDLFLRKSPTITGLVVDLAPSKGYNLWLSRASKPVNHSSTKEKONGTITVSTL 176
 Db 232 SFADIFLKSANLTCVLSNLATYE-TLINSWASOSGEPLETKIKIMSHPNRGTSANGVA 290
 QY 177 PVGTRDWEIEETQCYRTHLPHLALMRSTYKTSGPRAAEVYAFATP--EMPGRDKRT 234
 Db 291 SVCEEDNNKKEFKYCTYTHDLPSPQKFLSKREYVHKHPAYLLPRAEQLNRESAT 350
 QY 235 LACTIQNFMPEDISVQWLHNEVQLPDARHSTTPRKTGS-GF-FVFSRLVYRAWEOK 292
 Db 351 VTCLVKGFSPADISVQWLQGLLPQKRYVTSAPMPGAPGFYFHSILTVTEEWNSG 410
 QY 293 DEFICRAVHEAASPTQVQAVSNPK 320
 Db 411 ETVYGVGHERL-PHLYTERTVDKSTGK 437
 RESULT 5
 MUCM_MOUSE
 ID MUCM_MOUSE STANDARD; PRT; 476 AA.
 AC P01873;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Iq mu chain C region membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 433-476 FROM N.A.
 RX MEDLINE-80222874; PubMed-6771020;
 RA Early P., Rogers J., Davis M., Calame K., Bond M., Wall R.,
 RA Hood L.;
 RT "Two mRNAs can be produced from a single immunoglobulin mu gene by
 alternative RNA processing pathways.";
 RL Cell 20:313-319(1980).
 RN [2]
 RP SEQUENCE OF 410-476 FROM N.A. (MYELOMA MOPC 104E).
 RX MEDLINE-80222873; PubMed-6771019;
 RA Rogers J., Early P., Carter C., Calame K., Bond M., Hood L.,
 RA Wall R.;
 RT "Two mRNAs with different 3' ends encode membrane-bound and secreted
 forms of immunoglobulin mu chain.";
 RL Cell 20:303-312(1980).
 CC -1- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
 SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
 CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
 TERMINAL SEGMENTS.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-409 IS ASSUMED TO BE
 IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
 CC -----
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 DR EMBL; V00821; CAA24202.1; -;
 DR PIR; A02167; MHMS.

DR HSSP; P01857; 1fcl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00410; Ig_Like; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 105 CH1.
FT DOMAIN 106 217 CH2.
FT DOMAIN 218 324 CH3.
FT DOMAIN 325 436 CH4.
FT TRANSMEM 456 473 POTENTIAL.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 28 89
FT DISULFID 136 199 BY SIMILARITY.
FT DISULFID 216 216 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 246 305 BY SIMILARITY.
FT DISULFID 293 293 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 353 415 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 476 AA; 52656 MW; 80476575A5204071 CRC64;

Query Match 25.2%; Score 430.5; DB 1; Length 476;
Best Local Similarity 32.3%; Pred. No. 3.7e-27;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTVKLISSCG-GGHPPTTOLLVSGYPTGNTINIMLEGGQVMDVLSASTQGE 62
DB 112 PNVAVFVPSRDAFSGPAPKRSRLICEAFNEFTPKPLTVSMKLGKVGSGFTDPVTIEK 171
QY 63 LASTO-----SELTLSOKHMLSDRTYTCOVYQGHF-EDSKKCADSNPRGSAVLSRP 116
DB 172 GSTPQTYKVIISLTITSELDWMLNLYTCRVDRHGLTFKKNVSTCAASSTDIQAFPIRP 231
QY 117 SPFDLFIKSPPTITGLVVDLAPSKGTVNLTWASRASKPVNHSRREKORNGTLTVSTL 176
DB 232 SFADLFIKSKANLTLVSNLAHYE-TLNIWSASGSEPLETKIKIMESHNGTFSAGVA 290
QY 177 PVTGTDWIMEGTYOCRVTHPHLPRALMRSTTKTSGPRAPRYAATP--EWPGRDKRT 234
DB 291 SYCVEDMNNRKEFVTVTHRDLPSPQKFKISKPNVHKHPRAVYLLPPAREQLNRESAT 350
QY 235 LACLIONFMPEDISVQMLHNEVOLDPARHSTTOPRKTGS-GF-FVFSRLLEVTRAWECK 292
DB 351 VTCLVKGFSPADISVQMLORQGLPQEKYVTSAPMRPGAPRFYTHSLITVTEEMNGC 410
QY 293 DEFICRAVHEASPSQTVORAV 314
DB 411 EYTCVVGHEAL-PHLVTERTV 431

RESULT 6
MUC_MESAU
ID MUC_MESAU STANDARD; PRT; 454 AA.
AC P06337;
DT 01-JAN-1988 (rel. 06; Created)
DT 01-FEB-1996 (rel. 38; Last sequence update)
DT 15-JUL-1999 (rel. 38; Last annotation update)
DE Ig mu chain C region.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_Taxid=10036;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=85297761; PubMed=2994005;
RA McGuire K.L., Duncan W.R., Tucker P.W.;
RT "Phylogenetic conservation of immunoglobulin heavy chains: direct
RT comparison of hamster and mouse Cmu genes."
RT Nucleic Acids Res. 13:5611-5628(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X02804; CAA26574.1; -
DR PIR; A02168; MHY.
DR HSSP; P01854; 1fcl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00410; Ig_Like; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
KW NON_TER 1
KW DOMAIN 1 105 CH1.
KW DOMAIN 106 218 CH2.
KW DOMAIN 219 324 CH3.
KW DOMAIN 325 454 CH4.
KW DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
KW DISULFID 27 88 BY SIMILARITY.
KW DISULFID 135 198 BY SIMILARITY.
KW DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
KW DISULFID 245 304 BY SIMILARITY.
KW DISULFID 292 292 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
KW DISULFID 352 414 BY SIMILARITY.
KW CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 454 AA; 50196 MW; 4DA2134612BE1469 CRC64;

Query Match 24.8%; Score 423.5; DB 1; Length 454;
Best Local Similarity 31.5%; Pred. No. 1.3e-26;
Matches 106; Conservative 56; Mismatches 145; Indels 29; Gaps 10;

QY 4 PTVKLISSCG-GGHPPTTOLLVSGYPTGNTINIMLEGGQVMDVLSASTQGE 62
DB 111 PNVAVFVPSRDAFSGPAPKRSRLICEAFNEFTPKPLTVSMKLGKVGSGFTDPVTIEK 170
QY 63 LASTO-----SELTLSOKHMLSDRTYTCOVYQGHF-EDSKKCADSNPRGSAVLSRP 116
DB 171 GSGPRTYKVIISLTITSELDWMLNLYTCRVDRHGLTFKKNVSTCAASSTDIQAFPIRP 230
QY 117 SPFDLFIKSPPTITGLVVDLAPSKGTVNLTWASRASKPVNHSRREKORNGTLTVSTL 176
DB 231 SFVGIFLKNASATLTLVNLATYDPLNLSWSRSGSEPLETKIKIMESHNGTFSAGVA 289
QY 177 PVTGTDWIMEGTYOCRVTHPHLPRALMRSTTKTSGPR-----AAPRYAATPFWGSRDK 232
DB 290 NVCVEDMWSGKEFVTVTHRDLPSPQKFKISK--PREMNKTPPAVY-----QDPLARQ 341
QY 233 -----RTLACLIONFMPEDISVQMLHNEVOLDPARHSTTOPRKTGS--FVFSRLLEV 284
DB 342 LILRESATVTCVKGFSPPADISVQMLORQGLPQEKYVTSAPMRPGAPRPHLYFTSVLTV 401
QY 285 TRAEWQKDEFICRAVHEASPSQTVORAVSNPK 320

Db 402 TEEMNGSEITYTCVGHDL-PHNVETKVDKSTGK 436

RESULT 7

GC2_HUMAN STANDARD: PRT: 326 AA.

AC P01859; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ig gamma-2 chain C region.

GN IGHG2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid:9606;

RN [1]

RP SEQUENCE OF 2-326 FROM N.A.

RX MEDLINE=82197621; PubMed=6804948;

RA Ellison J.W., Hood L.E.;

RT "Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";

RT Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).

RL [2]

RP SEQUENCE OF 88-115 FROM N.A.

RX TISSUE-Fetal liver;

RX MEDLINE=83001943; PubMed=6811139;

RA Takahashi N., Ueda S., Obata M., Nakai S., Honjo T.;

RT "Structure of a human immunoglobulin gamma genes: Implications for evolution of a gene family.";

RT Cell 29:671-679(1982).

RL [3]

RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.

RX TISSUE-Fetal liver;

RX MEDLINE=8423592; PubMed=6329676;

RA Krawinkel U., Rabbits T.H.;

RT "Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";

RT EMBO J. 1:403-407(1982).

RL [4]

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).

RX MEDLINE=81007873; PubMed=6774012.

RA Wang A.-C., Tung E., Fudenberg H.H.;

RT "The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";

RT J. Immunol. 125:1048-1054(1980).

RL [5]

RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).

RX MEDLINE=80001357; PubMed=113080;

RA Connell G.E., Parr D.M., Hofmann T.;

RT "The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";

RT Can. J. Biochem. 57:758-767(1979).

RL [6]

RP SEQUENCE OF 238-275 (ZIE).

RX MEDLINE=80114419; PubMed=118920;

RA Hofmann T., Parr D.M.;

RT "A note of the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.";

RT Mol. Immunol. 16:923-925(1979).

RL [7]

RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).

RA Hofmann T., Parr D.M.;

RL Submitted (MAR-1980) to the PIR data bank.

RN [8]

RP SEQUENCE OF 1-121 (DOR).

RX MEDLINE=9525296; PubMed=7737190;

RA Scoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;

RT "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";

RT Eur. J. Biochem. 228:886-893(1995).

RN [9]

RP DISULFIDE BONDS.

RX MEDLINE=72033500; PubMed=4940472;

RA Mistein C., Frangione B.;

RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";

RL Biochem. J. 121:217-225(1971).

RN [10]

RP DISULFIDE BONDS.

RX MEDLINE=69064124; PubMed=5782707;

RA Frangione B., Mistein C., Plink J.R.L.;

RT "Structural studies of immunoglobulin G.";

RL Nature 221:145-148(1969).

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CC EMBL: J00230; AAB59393.1; -

DR PIR: A02148; G2HU.

DR HSSP: P01857; IRL1.

DR Genew: HGNC:5526; IGHG2.

DR MIM: 147110; -

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003597; Ig_c1.

DR InterPro: IPR003600; Ig_Like.

DR Pfam: PF00047; Ig_3.

DR SMART: SM00407; Ig_Like; 1.

DR SMART: SM00407; Ig_c1; 2.

DR PROSITE: PS00290; Ig_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1 1

FT DOMAIN 99 110

FT DOMAIN 111 219

FT DOMAIN 220 326

FT DISULFID 14 14

FT DISULFID 27 83

FT DISULFID 102 102

FT DISULFID 103 103

FT DISULFID 106 106

FT DISULFID 109 109

FT DISULFID 140 200

FT DISULFID 246 304

FT SITE 156 156

FT MOD_RES 326 326

FT VARIANT 60 60

FT CONFLICT 109 109

FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

SO

Query Match 24.4%; Score 416; DB 1; Length 326;

Best Local Similarity 31.28; Pred. No. 3,4e-26;

Matches 105; Conservative 59; Mismatches 136; Indels 36; Gaps 11;

QY 11 SSCDGGGHP-----PTIQLCLVAGYPTGNTINLEDDGYVDVLDASTTQ 60

DB 1 ASKRGSPVFLPLACSRSTSESTALGCLVADYFPEPTVSM-NSGALTSGVHFPAYLOS 59

QY 61 GELASTQSELTLSOKHMLSDRTYTCQVYQ-GHTEEDST--KKCADSNP-----RGVS 110

DB 60 SGLYSLSSVTVPSNFG-GRQYTCNDVHDKPSNTKVTBRKCCVCEPCPPAPVAGPS 118

QY 111 AYLSRSPSPD-LPIKSPITITCLVADLPASKGYNLTWASAGSKPVVHSTRKEKQRNGT 169

DB 119 VFLEPPKPKDPTLMSIRPEVTCVVDVSHDPEQFMWYDGVHNAKTRPREDFNST 178

QY 170 LVTSTLPVGTGRMIEGETYQCRTHPLPALMRSTKSGRAAEVYAFATPEWPGS 229

DB 179 FRVVSUTLVVHOMLNKKEKCKVSNKGLPALEKTIKTKGQPREQVYTL-----PPS 233

QY 230 RDKRT-----LACLIQNFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFEVFSRLV 284
 DB 234 REENTKNQVSLTCLVKCFEYPSDLAVESN--GGPENNYKTTTPMDSDSFLYSLTY 291
 QY 285 TRAEWECKDEFFICRAVHEAASPSQTVORAVSVNPGK 320
 DB 292 DKSRMOOGNVCFSVMHEALHNHYT-OKSLSLSPGK 326

RESULT 8
 MOC_SUNMU
 ID MOC_SUNMU STANDARD; PRT; 457 AA.
 AC P20768;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 1g mu chain C region.
 OS Suncus murinus (House shrew) (Musk shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.
 NCBI_TaxID=9378;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89232144; PubMed=2497033;
 RA Ishiguro H., Ichihara Y., Namikawa T., Nagatsu T., Kurosawa Y.;
 RT "Nucleotide sequence of Suncus murinus immunoglobulin mu gene and
 RL comparison with mouse and human mu genes.";
 FEBS Lett. 247:317-322(1989).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X13920; GAA32113.1; ALT_INT.
 DR PIR: S03961; S03961.
 DR HSSP; P01842; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; IgC1; 3.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 105 CH1.
 FT DOMAIN 106 220 CH2.
 FT DOMAIN 221 326 CH3.
 FT DOMAIN 327 457 CH4.
 FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
 FT DISULFID 27 89 BY SIMILARITY.
 FT DISULFID 136 200 BY SIMILARITY.
 FT DISULFID 217 217 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 248 307 BY SIMILARITY.
 FT DISULFID 295 295 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 355 417 BY SIMILARITY.
 FT DISULFID 456 456 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 457 AA; 50074 MW; 56C8C086DA4462E9 CRC64;

Query Match 24.2%; Score 413.5; DB 1; Length 457;
 Best Local Similarity 30.1%; Pred. No. 8; le-26;

Matches 100; Conservative 58; Mismatches 157; Indels 17; Gaps 9;
 QY 3 PPTVKLIQSSDCD-GGHFPTLIOLCLVSGTGTINITWLEGGQVMDVLSASTQEG 61
 DB 111 PPNVSLFVPPRNSESGNHPRTSOLICQASFSPTITWMLQKEPQPSLVSAYEAE 170
 QY 62 ELAS-----TOSELTLQKHWLSDRTYTOQVVOYQGHFTPDSTKK--CADSNRGVAYL 113
 DB 171 PKSGPTTFRVISRLTTEENWLSQREFTOALAKGLTFPKNNVSVCMGSDTSTGISVFL 230
 QY 114 SRSPFDLPTFKSPFTITCLVVDLAPSKGYVNLWVSRAKSPVNHSTRKEKQNGTLTYT 173
 DB 231 LPPTFANIFLTQSOLCLVTGLA-TYDSIDISWRONGEALQTHVNISESHNSTPTAK 289
 QY 174 STLPVGRDWIEGTEYOCRTYTHPLPRALKRSTTKSG-PRAPPEYAF-ATPEMGSRD 231
 DB 290 GHASVCREEWSGKEKFTYQHSDDLPSLKQSLSRPKVDANDPVSFVLPRPQEQKLRE 349
 QY 232 KRTLACLIQNFMEDISVQWLHNEVOLPDARHSTTQ---PRKTKSGFEVFSRLVRAE 288
 DB 350 SASITCLVKPSPDPVQVQHHG-QPVDPKHVYTSNPTPEPQNGIFYHSLITVSEKD 408
 QY 289 WEQKDEFFICRAVHEAASPSQTVORAVSVNPGK 320
 DB 409 WSSGSEFSFCVVGHEAL-PLSVTERKAVDKTSGK 439

RESULT 9
 MOCB_HUMAN
 ID MOCB_HUMAN STANDARD; PRT; 391 AA.
 AC P04220;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 1g mu heavy chain disease protein (BOT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=84184186; PubMed=6425189;
 RA Barnikol-Watanabe S., Mihaesco E., Mihaesco C., Barnikol H.U.,
 RA Hilschmann N.;
 RT "The primary structure of mu-chain-disease protein BOT. Peculiar
 RL amino-acid sequence of the N-terminal 42 positions.";
 HL Hoppe-Seyler's Z. Physiol. Chem. 365:105-118(1984).
 CC -i- MISCELLANEOUS: THIS PROTEIN HAS NO V REGION HOMOMOLOGY OR CH1
 CC REGION.
 DR PIR: A02163; MHHDUT.
 DR HSSP; P01857; IFCL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; IgC1; 2.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT DOMAIN 1 42 PRE-C-PAET (NO V REGION HOMOMOLOGY).
 FT DOMAIN 43 155 CH2.
 FT DOMAIN 156 261 CH3.
 FT DOMAIN 262 391 CH4.
 SO SEQUENCE 391 AA; 43057 MW; 9100843AF0CF021A CRC64;

Query Match 24.0%; Score 410; DB 1; Length 391;
 Best Local Similarity 28.6%; Pred. No. 1.3e-25;
 Matches 95; Conservative 61; Mismatches 156; Indels 20; Gaps 9;
 QY 3 PPTVKLIQSSDCGGHPPTIQLCLVSGTGTINITWLEGGQVMDVLSASTQEG 62
 DB 48 PPKVSVFVPPRDGFGNPNRKRSLICQATGSPROIETVSWLRGK-----QVGSVTTDEVE 103

OY 63 LASTO-----SELTSOKHMLSDRTYTCOVYOGHTF-EDSTKCKADSNPGVSAY 112
 DB 104 AEARESGPTTYKVTSTLIKESDWMGOSMTCRDVHRLTFOQNASMCGPDODTALVVF 163
 OY 113 LSRSPFDLFRKSPPTICLVADLAPSKGVNLWTSRASKGPNVHSTRKEKORNGTLTV 172
 DB 164 AIPPSFASIFLTKSKTKLCLVTDLT-TYDSVTISMTRODGAVKHTHTISSHPNATPSA 222
 OY 173 TSTLPVGTDMIESEPTVOCRVTHPLPALMRSTTKTSGPRA-APEVYAF-ATPEWPGSR 230
 DB 223 VGEASICEDWDMSGERFTCYTHDLPSPKOTISRPKGVALLHRPDVYLLPPARQULNR 282
 OY 231 DKRLACLIONFMEDISVQVLNHEVQLPDARHSTQPR-KTKSGG-FEVSRLVETPAE 288
 DB 283 ESAITTCVLTGFSPADVFWQWMOGQPIISPPEKYTSAPMPPOAPGRYFAHSILTVSEEE 342
 OY 289 WEORDEFICRAVHEAASPSQTVORAVSNPCK 320
 DB 343 WNTGETYCVVAHNEAL-PNRYTERTVDSKSTCK 373
 RESULT 10
 MOC_HUMAN STANDARD: PRF: 454 AA.
 ID AC P01871;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ig mu chain C region.
 GN IGHM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-434 FROM N.A.
 RA MEDLINE=90332450; PubMed=2115996;
 RA Friedlander R.M., Nussenzweig M.C., Leder P.;
 RT "Complete nucleotide sequence of the membrane form of the human IgM
 RT heavy chain.";
 RL Nucleic Acids Res. 18:4278-4278(1990).
 RN [2]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN GAL).
 RA MEDLINE=75059123; PubMed=4803843;
 RA Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 RT (macroglobulin gal.), II: the amino acid sequence of the H-chain (mu-
 RT type), subgroup H III. Architecture of the complete IgM-molecule.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN [3]
 RP REVISIONS (GAL).
 RA MEDLINE=81066716; PubMed=6777162;
 RA Milhaesco E., Barnikol-Watanabe S., Barnikol H.U., Milhaesco C.,
 RA Hilschmann N.;
 RT "The primary structure of the constant part of mu-chain-disease
 RT protein B0F.";
 RL Eur. J. Biochem. 111:275-286(1980).
 RN [4]
 RP SEQUENCE (WALDENSTROM'S 00), DISULFIDE BONDS, AND CARBOHYDRATES.
 RA MEDLINE=74005511; PubMed=4742735;
 RA Putnam F.W., Florent G., Paul C., Shinoda T., Shlimizu A.;
 RT "Complete amino acid sequence of the mu heavy chain of a human IgM
 RT immunoglobulin.";
 RL Science 182:287-291(1973).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A.
 RA MEDLINE=82059479; PubMed=6795593;
 RA Rabbitts T.H., Forster A., Milstein C.P.;
 RT "Human immunoglobulin heavy chain genes: evolutionary comparisons of
 RT C mu, C delta and C gamma genes and associated switch sequences.";
 RL Nucleic Acids Res. 9:4509-4524(1981).
 RN [6]
 RP SEQUENCE OF 299-387 AND 438-454 FROM N.A.

RX MEDLINE=81077306; PubMed=6777778;
 RA Dobly T.W., Deviano J., Croce C.M.;
 RT "Cloning and partial nucleotide sequence of human immunoglobulin mu
 RT chain cDNA from B cells and mouse-human hybridomas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).
 CC -I- MISCELLANEOUS: ALL 4 COMBINATIONS OF THE S/G & V/G POLYMORPHISMS
 CC AT POSITIONS 192 AND 216 HAVE BEEN OBSERVED IN HUMAN MU CHAINS.
 CC -----
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 CC -----
 DR EMBL: X17115; CAA34971.1; ALT SEQ.
 DR EMBL: X57086; -: NOT_ANNOTATED_CDS
 DR PIR: A02162; MHU.
 DR HSSP: P01857; IFC1.
 DR GeneW: HGNC:5541; IGHM.
 DR MIM: 147020;
 DR GlycosultEDB: P01871;
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003600; IG-like.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00410; IG-like; 1.
 DR SMART: SM00407; IGH; 3.
 DR PROSITE: PS00290; IG_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1
 FT DOMAIN 1
 FT DOMAIN 106 105
 FT DOMAIN 219 218
 FT DOMAIN 325 324
 FT DOMAIN 325 454
 FT DISULFID 14 14
 FT DISULFID 28 88
 FT DISULFID 135 198
 FT DISULFID 215 215
 FT DISULFID 245 304
 FT DISULFID 292 292
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN IN ANOTHER
 FT OF THE 5 TETRAMERIC SUBUNITS OF THE
 FT MOLECULE).
 FT DISULFID 352 414
 FT DISULFID 453 453
 FT CARBOHYD 46 46
 FT CARBOHYD 210 210
 FT CARBOHYD 273 273
 FT CARBOHYD 280 280
 FT CARBOHYD 441 441
 FT VARIANT 192 192
 FT VARIANT /FTID=VAR_003903.
 FT VARIANT 216 216
 FT VARIANT /FTID=VAR_003904.
 FT SEQUENCE 454 AA; 49556 MW; 21EC72EADC56922E CRC64;
 SQ
 Query Match 23.8%; Score 405.5; DB-1; Length 454;
 Best Local Similarity 28.6%; Pred. No. 3.5e-25;
 Matches 94; Conservative 64; Mismatches 158; Indels 13; Gaps 9;
 OY 3 PPTVYKLIQSSCDG-GGHEPPTIOLLCLVSGYTPGTINITWLEDQGVNDVLSASTQEG 61
 DB 110 PPKVSVFVPPRDGDFGNPRSKSLICQATGFSFPROIOVSWLREKQVSGVTTDOVAFA 169
 OY 62 ELA-----STQSELTLSQKMWLSDRITTCOVYOGHTF-EDSTKCKADSNPGVSAYLR 115
 DB 170 KESGPTTYKVTSTLIKESDWMGOSMTCRDVHRLTFOQNASMCGPDODTALVFAIP 229
 OY 116 PSPFDLFRKSPPTICLVADLAPSKGVNLWTSRASKGPNVHSTRKEKORNGTLTVTST 175
 DB 230 PSFASIFLTKSKTKLCLVTDLT-TYDSVTISMTRODGAVKHTHTISSHPNATPSA 288

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QY 176 LPVGTBDMIEGETYQCRVTHPHLRALMRSTKTSGRPA-APEVYAF-ATPEMFGSRDKR 233
D 289 ASIEDDMNSGERCTVTHDLPSPKQITSRKGVALLHPDYLPPAREQNLRESA 348
QY 234 TLACIIONMPEIDISVOMLHNEVOLPDARHSTTOPR-KTKGSG-FEVSRLRYRAREQ 291
D 349 TITLVGFSPADVFVOMQOPLSPKRYTSPADMPBPAPGRYFAHSILTVSEEWNT 408
QY 292 KDEFCIRAVHEASPSQTVQRAVSVPNGK 320
D 409 GETTCVAHEAL-PNRYTERTVDKSTGK 436

RESULT 11
MUC_RABIT STANDARD: PRT: 458 AA.
ID MUC_RABIT STANDARD: PRT: 458 AA.
AC P03988:
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (A2 ALLOTYPED).
RX MEDLINE=84088930; PubMed=6418803;
RA Bernstein K.E., Alexander C.B., Reddy E.P., Mage R.G.;
RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
  of Vha2 allotype: comparisons with Vha1 and membrane mu sequences.";
RL J. Immunol. 132:490-495(1984).
CC -1- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
  SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
  TERMINAL SEGMENTS.
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  entities requires a license agreement (See http://www.isb-sdb.ch/announce/
  or send an email to license@sdb.ch).
CC -----
DR EMBL: K01357; -; NOT_ANNOTATED_CDS.
DR PIR: A02164; MHRB.
DR HSSP: P01842; 7PAR.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_4.
DR SMART: SMO0410; Ig_Like; 2.
DR SMART: SMO0407; Ig_Like; 2.
DR PROSITE: PS00290; Ig_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 106 CH1.
FT DOMAIN 107 222 CH2.
FT DOMAIN 223 327 CH3.
FT DOMAIN 328 458 CH4.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 28 90 BY SIMILARITY.
FT DISULFID 137 200 BY SIMILARITY.
FT DISULFID 219 219 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 249 308 BY SIMILARITY.
FT DISULFID 296 296 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 356 418 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 458 AA; 49897 MW; F338D6A328E4864 CMC64;

Query Match 23.8%; Score 405.5; DB 1; Length 458;
Best Local Similarity 30.0%; Pred. No. 3.6e-25;
Matches 100; Conservative 60; Mismatches 154; Indels 19; Gaps 10;

QY 3 PPTVKIL---QSSDGGGHPPTIQLCLVSGYRGNTINLWDGGVMDVLTASTQ 59
D 112 PPNVSVFLPPRDSGSG--TRKSLICQATGSEKQISWLDGQKVEGVLTKPYEA 169
QY 60 EGELA-----STQSELTLQKQKMLSDRTYTCQVYQGHTEFDS--TKKCADSNRGVSA 111
D 170 ETKGAPATFESSMLTFTESDWLSQSLYTCRVDRHGRIFFPKNYSMSSECTTSPGIQV 229
QY 112 YLSRSPEDLFIKRSPTTCLVLDLASKGTVNTLWTSASGKPVNHSRKEKORNGTLT 171
D 230 FPIAPSPADTFLSKRSARLICLVDTLT--TYSGLNISMASHNGKADTHNITESHNPATFS 288
QY 172 VTSTLPVGTBDMIEGETYQCRVTHPHLRALMRSTKT-SGPRAAPEVYAF-ATPEMFGS 229
D 289 AMGEASVCAEDWESGEQFTCTVTADLPFLKHTITSREYAKHPAPVYULPAREQLVL 348
QY 230 RDKRTLACIIONMPEIDISVOMLHNEVOLPDARHSTTOPR-KTKGSG-FEVSRLRYRA 287
D 349 RESATVETCLVGFSPADVFVOMQOGLSSDKTYTSAPAPBPAPGLYFHSILTVTEE 408
QY 288 EWEQKDEFTCAVHEASPSQTVQRAVSVPNGK 320
D 409 DWNSEFTCVVGHLEAL-PNRYTERTVDKSTGK 440

RESULT 12
GC2_CAVPO STANDARD: PRT: 329 AA.
ID GC2_CAVPO STANDARD: PRT: 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
CC NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (Apr-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
  immunoglobulin-G(2). 3. Amino acid sequence of the region around the
  half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
  immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
  and hinge region cyanoogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
  antibodies.";

```

RL Biochemistry 13:4796-4803(1974).
 RN [5]
 RP SEQUENCE OF 227-311.
 RX MEDLINE-75036073; PubMed-4609467;
 RA Trischmann T.M., Cedra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 antibodies";
 RL Biochemistry 13:4804-4811(1974).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE-71058474; PubMed-4922544;
 RA Oliveira B., Lam M.E.;
 RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
 RL Biochemistry 10:26-31(1971).
 CC -1 MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
 CC 13 INBRED GUINEA PIGS.
 DR PIR: A02151; GZGP.
 DR HSSP: P01842; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1
 FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 28 79
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 142 202
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
 FT DISULFID 248 308
 SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;
 Query Match 23.7%; Score 404.5; DB 1; Length 329;
 Best Local Similarity 30.6%; Pred. No. 2.8e-25;
 Matches 106; Conservative 56; Mismatches 135; Indels 49; Gaps 13;
 QY 2 TPPTVYKILQSSC-DGGGHFPPTIQLCLVSGYPTGNTITWLEDGQVNDVLDSTASTQ 60
 DB 5 TAPSVFPLAASCVDYSGSM--MTLGLVKGYPPEPVVKM--NSGALTSVTHFPAVLQ 59
 QY 61 GELASTOSELTLGSKHMLSDRTYCOVLYOCHTFEDSK-----KC 101
 DB 60 SGLYSLISMVTP-----SSQKATCVNAHPA-----STKVDKTVPIRTZPBPCTCPKC 110
 QY 102 -ADSNPRGVSAYLSRPSFPD-LFIRKSPITCLVVDLAPSKGTNLTWRSRSGKPY-NHS 158
 DB 111 PRPENLGGPSVFIFPPPKDILMISLPRTVCVVVDVSDPEVQFTWF-VDNKPVGNAL 169
 QY 159 TRKEKQRNGTLIVTSLPVGTRDMIGETVYQCRVTHPLPALMRSTTKTSGPRAPEV 218
 DB 170 TKPRVEDQYNTTFVESVLPLOHODMLRGEKCKYVKALPAPLEKTIKTKGAPRMDV 229
 QY 219 YAFATPMPGSRD-----KRTLACLIONFMEPDISVOMLHNEVOLDPAKHSHTQPKTKG 273
 DB 230 YTL-----PSRDLKSKVSVTLILNFPPADLHVEWASRYVSVSEKKNTPEIDAD 284
 QY 274 SGFEVSRLEVTYRAEMOKDEFICRAVHEAASPQFORAVSVPG 319
 DB 285 GSYFLYSLKLVYDKSAMQGTIVYTCVSHALH-NHYTOKAISRSPG 329

DE Ig gamma-1 chain C region.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-80045036; PubMed-115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE-80202559; PubMed-6769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
 cloned in a bacterial plasmid.";
 RL Gene 9:87-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE-80012837; PubMed-113776;
 RA Rogers J., Clarke P., Salsler W.;
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
 heavy chain.";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE-78242288; PubMed-98524;
 RA Adeltubo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 murine myeloma gamma1 chain.";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE-73008889; PubMed-5073237;
 RA Svastli J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
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 CC -----
 DR EMBL: V00793; CAA24172.1; -
 DR EMBL: V00793; CAA24173.1; -
 DR EMBL: V00793; CAA24174.1; -
 DR EMBL: V00793; CAA24175.1; -
 DR EMBL: V00795; CAA24176.1; -
 DR PIR: A02159; GIMS.
 DR HSSP: P01842; 7FAB.
 DR GlycoSuiteDB: P01868; -
 DR MGD: MGI:96446; Igh-4.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig-cl.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1
 FT DOMAIN 1 97
 FT DOMAIN 98 110 CH1.
 FT DOMAIN 111 217 HINGE.
 FT DOMAIN 218 324 CH2.
 FT DISULFID 27 82 CH3.
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).

	FT	DISULFID	104	104	INTERCHAIN (WITH A HEAVY CHAIN).
	FT	DISULFID	107	107	INTERCHAIN (WITH A HEAVY CHAIN).
	FT	DISULFID	109	109	INTERCHAIN (WITH A HEAVY CHAIN).
	FT	CARBOHYD	138	198	N-LINKED (GLCNAC. . .),
	FT	CARBOHYD	174	174	/FTID-CAR_000055.
	FT	DISULFID	244	302	
	FT	MOD RES	324	324	REMOVED POST-TRANSLATIONALLY.
	FT	CONFLICT	276	276	N-> D (IN REF. 3).
	FT	CONFLICT	278	278	N-> D (IN REF. 3).
SQ	SEQUENCE	324 AA;	35704 MM;	A338812F3D1FC93 CRC64;	
	Query Match		23.6%;	Score 402;	DB 1:
	Best Local Similarity		29.2%;	Pred. No. 4,4e-25;	Length 324;
Matches	96;	Conservative	60;	Mismatches	155; Indels 18; Gaps 7.
QY	2	TPTPVKILIQSSCDGGHFPPIYLQLCLVSGVTGPTINTITWLEDGVMDVDISTASTGTQEG	61		
Dd	4	TPPSVVPPLAP--SAAOTNSMWTLLGLCKVGFEPEVTVTW--NSSLSSGHTPFAVLQS	59		
QY	62	EIASTOSELTLISQKHMLSDRTNYTGYMYQHGF-----EDGTKCAQSNPNPGVAX	112		
Dd	60	DLYLSSSVIYPSSPRSE-TVTCNAVPAASSTKYDKATVPPDCGKCPCICIVPEVSVF	118		
QY	113	LSRSPDP-LFIKRSPTITLCVLDVLAIPSKGTVINLTWSRASGKPWNHSSTRKEBKONGTLT	171		
Dd	119	IIFPKRPKDVLITLTPKVTCVVNDISKDDPEVGSWFVDVEVHTAQNPREGENSTFR	178		
QY	172	VTSLPVGRKWIGETYYQCAYTRPHLRALMRSTTKTSGRAAEVAFAFEPWGSRD	231		
Dd	179	SVSLEPIPMHOHWLGMEKFKCVNSAAPAFPLEKTITSKGRRKAPOVYTTPPPKKDMKD	238		
QY	232	KRTIACLIONMPMEDISVOYMLHNEVOLDEDAHSTTOPKRTGSGGFVESRLVTRAEMEQ	291		
Dd	239	KVSLCTMTDFEFDIYTEMQN--GPAAENVKNQPIIMNTNGSFYFSKLNVOKSMNMA	296		
QY	292	KDEFICRAVHEAASPQTORAVSYNPCK	320		
Dd	297	GNETCGSYLMHGHLNNHMT-EKSLSHPSPK	324		
	RESULT 14				
	GCAA_MOUSE	STANDARD:	PRT:	330 AA.	
AC	P01863;				
Dt	21-JUL-1986 (Rel. 01, Created)				
Dt	21-JUL-1986 (Rel. 01, Last sequence update)				
Dt	30-MAY-2000 (Rel. 39, Last annotation update)				
De	Ig gamma-2A chain C region, A allele.				
Os	Mus musculus (Mouse).				
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Oc	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
Ox	NCBI_Taxid=10090;				
Rn	[1]				
Rp	SEQUENCE FROM N.A.				
Rx	MEDLINE=81076554; PubMed=6777755;				
Rt	SIKOBY J.-L., Aufray C., Rougeon F.;				
Rt	"Structure of the constant and 3' untranslated regions of the murine				
Rl	Balb/c gamma 2a heavy chain messenger RNA."				
Rn	Nucleic Acids Res. 8:3143-3155(1980).				
Rn	[2]				
Rp	SEQUENCE FROM N.A.				
Rx	MEDLINE=81198976; PubMed=6262729;				
Rt	Yanawaki-Katsuka Y., Miyata T., Honjo T.;				
Rt	The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene				
Rt	and evolution of heavy chain genes: further evidence for intervening				
Rt	sequence-mediated domain transfer.";				
Rl	Nucleic Acids Res. 9:1365-1381(1981).				
Rn	[3]				
Rp	SEQUENCE FROM N.A.				
Rx	MEDLINE=81223894; PubMed=6787604;				
Rt	Ollio R., Aufray C., Morchamps C., Rougeon F.;				
Rt	*Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes				

suggests that exons can be exchanged between genes in a multigenic family.";

[4]
Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).

RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Cc fragment. Implications for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]

RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).

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DR EMBL: V00798; CAA24178.1; -
DR PIR: A02152; GZMSA.
DR HSSP: P01842; TPAB.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003597; IG_CL.
DR InterPro: IPR003600; IG_LIKE.
DR Pfam: PF00047; IG_2.
DR SMART: SM00410; IG_LIKE_1.
DR SMART: SM00407; IGLI_2.
DR ProSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFD 15 15
FT DISULFD 27 82
FT DISULFD 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 144 204
FT DISULFD 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CMC64;

Query Match 23.4%; Score 399; DB 1; Length 330;
Best Local Similarity 28.6%; Pred. No. 7.8e-25;
Matches 97; Conservative 62; Mismatches 148; Indels 32; Gaps 8;

Dy 2 TPTVTKIQSCDCGGHPPITOLLCLVSGTPGTINTWLEDQGVMDVDISTASTQEG 61
| | : : : : : | | : : : : : | | : : : : : | | : : : : : |
4 TAPSVPLAPPC--GDITGSSVTIGCLVKGIFFPEPVITM--NGSGLSGVHTPAVLQS 59
| | : : : : : | | : : : : : | | : : : : : | | : : : : : |
Dy 62 ELASTOSELLISOKHWLSIDRTYTQVITYQGHTFEDSTKCADSNRGVSA----- 111
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 60 DLYTLSSSVTVTSSTWPS-QSITCNVAHPA----SFTVKDKIEBPGPTIKRPPCKCPA 114
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Dy 112 --YLSRSPF-----DLFKRSPTITCLVLDLAPSKGVNLTWASASKPVNHSRK 161
| | : : : : : | | : : : : : | | : : : : : | : : : : : | : : : : : |
Db 115 PNLLGSGVEFPFRKIDVLMISPIYTCVVVDSEDDPDVQISWEFNANNEVHTAQOT 174
| | : : : : : | | : : : : : | | : : : : : | : : : : : | : : : : : |
Dy 162 EEKORNGLTITSTLPVGTRDMIGETVQCCHVTHPLRALMRSTTKSGRAPAEVYAF 221
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 175 HREDYNSTRKRVASLPIDHQDMWGKEKKCVNNKNDLPARLERIISKKGSVRAPQVYL 234
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Dy 222 ATPPMGSROKRKTACLQIONMPEDISVOMLHNEYOLDARHSTTORPKTKGSGEYFSR 281
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 235 PPPEEMTKKOVTLTCVTDPMEDIVIEWTN--GKETELNYKNTEPELVSDSGSYFMYSK 292

OY 282 LEVTRAEWQKDEFCRAVHEAASPTQVQRAVSNPKK 320
 DB 293 LRVKKNVNRYSCSYVHEGLNHHHTT-KSFSTPKK 330
 RESULT 15
 GCL_HUMAN STANDARD: PRT: 330 AA.
 AC P01857;
 DC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DF 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-1 chain C region.
 GN IGHG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82274238; PubMed=6287432;
 RA Ellison J.W., Berson B.J., Hood L.E.;
 RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
 RL Nucleic Acids Res. 10:4071-4079(1982).
 RN [2]
 RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
 RX MEDLINE=71064024; PubMed=3489771;
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
 RA Waxdal M.J., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
 RL Biochemistry 9:3161-3170(1970).
 RN [3]
 RP SEQUENCE OF 136-329 (EU).
 RX MEDLINE=71064025; PubMed=5530842;
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 RA Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
 RL Biochemistry 9:3171-3181(1970).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN NIE).
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponsingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
 RT chymotryptic peptides of the H-chain, alignment of the tryptic
 RT peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=688494;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie). I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human IgG fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35, 116, 198, 269 & 272.
 CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 135, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198, 267 & 272.
 CC -----
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 CC -----
 DR EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A02146; GHU.
 DR PDB: 1FC1; 15-JUL-92.
 DR PDB: 1FC2; 15-JUL-92.
 DR GeneW: HGNC:5525; IGHG1.
 DR MIM: 147100; .
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; IgC1; 2.
 DR PROSITE: PS00290; Ig_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT FT NON_TER 1 1
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 FT FT CARBOHYD 180 180
 FT FT MOD_RES 330 330
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 FT FT VARIANT 239 239
 FT FT VARIANT 241 241
 FT FT STRAND 123 126
 FT FT HELIX 130 134
 FT FT TURN 136 137
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 FT FT STRAND 158 162
 FT FT TURN 163 164
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 FT FT HELIX 193 197
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 D -> E (IN GIM(NON-1) MARKER).
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Query Match 23.3%; Score 397.5; DB 1; Length 330;
Best Local Similarity 31.0%; Pred. No. 1e-24;
Matches 102; Conservative 54; Mismatches 138; Indels 35; Gaps 10;

QY 12 SCGGGHEPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGELASTOSELT 71
DB 17 STSGG-----TALGCLVKDYFPEPVTVSW-NSGALTSGVHTFPAVLQSSGLYSLSSVT 70
QY 72 LSKHMLSDRTYTCQYTYOCHTE-----DSTKRC-----ADSNPRGVSAIYLSRPS 117
DB 71 VPSSS-LGTQTYICNVNHNKPSNTRKVDKVEPKSCDKTHTCPCPAPPELLGGPSVFLP 129
QY 118 PFD-LFIRKSPITTCVLVDLAPSKGVNLTWSRASGKPVNHNSTRKEEKORNGTLTVSTL 176
DB 130 PKDTLMSRPEYTCVVDVSHEDPEYKFMWYDGVVHNAKTRPREQYINSTYRVSVL 189
QY 177 PVGTROMIEGETYOCRVTHPLPALMSTTKTSGPRAAPEVYAFAPEWPGSRDKRT-- 234
DB 190 TVLHODWLNGEKYCKSNKALPAPIETISKAKGPPEPOVYTL-----PPSRDELTKN 244
QY 235 ---LACLIQNPEDISVOMLHNEVQLDARHSTTOPRKTKSGSGFFVFSRLEVTRAEMEQ 291
DB 245 QVSLTCLVKGFFPSDLAVEMESN--GQPENNYKTPPVLDSDGSFELYSKLVKSRWOO 302
QY 292 KDEFFICRAVHEAASPSQTVORAVSVNPGK 320
DB 303 GNVFSCSVMHALHNHT-QKSLSLSPRK 330

Search completed: July 15, 2003, 06:58:20
Job time : 10.9911 secs

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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:46:49 ; Search time 37.6806 Seconds
(without alignments)
1131.621 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1707	100.0	323 AAU80284	Human IGE heavy ch
2	1707	100.0	323 AAU80285	Human IGE C2-C3-C4
3	1707	100.0	323 AAU80286	Human IGE C2-C3-C4
4	1707	100.0	324 AAR83525	Fc(epsilon) CH2'-C
5	1707	100.0	325 AAR75225	Human IGE Fc chain
6	1707	100.0	325 AAR77241	Human IGE Fc chain
7	1707	100.0	331 AAB03642	Human IGE heavy ch
8	1707	100.0	367 AAP80291	Interleukin-2/IGF
9	1707	100.0	428 AAU80283	Human IGE heavy ch
10	1707	100.0	428 AAM50940	Human IGE epsilon

11	1707	100.0	428 AAM47863	Human Ig-E heavy C
12	1701	99.6	325 AAU79994	Human immunoglobul
13	1696	99.4	336 AAU80288	Human IGE heavy ch
14	1696	99.4	441 AAU80287	Human IGE heavy ch
15	1693	99.2	493 AAP40065	Sequence of human
16	1685	98.7	325 AAR83582	CH2 to CH4 of huma
17	1677	98.2	315 AAR85599	Fc(epsilon) CH2'-C
18	1671	97.9	330 AAU80289	Human IGE C2-C3-C4
19	1663	97.4	428 AAR82582	Human IGE heavy ch
20	1158	67.8	218 AAR85583	Human IGE heavy ch
21	1158	67.8	222 AAG55599	Amino acid sequenc
22	1088	63.7	201 AAR85589	Fc(epsilon) CH2'-C
23	1038.5	60.8	342 AAU806205	Immunogenic peptid
24	1038	60.8	209 AAP90010	Residues 340-547 o
25	1013	59.3	190 AAR5584	Fc(epsilon) CH2'-C
26	948.5	55.6	426 AAR97753	Canine IGE. Canis
27	945	55.4	424 AAM50103	Equine IGE heavy C
28	943	55.2	424 AAM50104	Equine IGE heavy C
29	928.5	54.4	417 AAM23067	Canine IGE heavy C
30	895.5	52.5	312 AAU79995	Dog immunoglobulin
31	827	48.4	341 AAB06208	Immunogenic peptid
32	793	46.5	340 AAB03643	Rat IGE heavy chal
33	783	45.9	313 AAU79996	Rat immunoglobulin
34	781	45.8	341 AAB03644	Opossum IGE heavy
35	770	45.1	345 AAB06207	Immunogenic peptid
36	751	44.0	332 AAU80297	Immunogenic peptid
37	751	44.0	332 AAU80298	Murine IGE heavy ch
38	751	44.0	332 AAU80299	Murine IGE heavy C
39	751	44.0	341 AAB06206	Immunogenic peptid
40	751	44.0	421 AAU80300	Murine IGE heavy ch
41	748	43.8	343 AAU80295	Murine IGE heavy C
42	748	43.8	343 AAU80296	Murine IGE heavy C
43	748	43.8	432 AAU80294	Murine IGE heavy C
44	695	40.7	130 AAR85585	Fc(epsilon) CH2'-C
45	691.5	40.5	313 AAU79997	Mouse immunoglobul

ALIGNMENTS

RESULT 1	AAU80284	standard; Protein: 323 AA.
ID	AAU80284	
XX	AAU80284	
AC	AAU80284	
XX	30-JUL-2002	(first entry)
XX	Human IGE heavy chain C2-C3-C4 domains.	
DE	Human IGE heavy chain C2-C3-C4 domains.	
XX	IGF: allergy; human; antiallergic; immunosuppressive; antiaphylactic;	
XX	antiallergic; dermatological; antiinflammatory; immunoglobulin E; IGE;	
KW	vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;	
KW	heavy chain C domain.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Domain	8..103 "Ige heavy chain C2 domain"
FT	Region	100..114
FT	Region	/note="Epitope including C2C3 linker"
FT	Region	104..111
FT	Domain	/note="Linker between domains C2 and C3"
FT	Region	112..211
FT	Region	/label="Ige heavy chain C3 domain"
FT	Region	139..145
FT	Region	/note="Epitope in BC loop"
FT	Region	167..175
FT	Region	/note="Epitope in DE loop"
FT	Domain	196..206
FT	Region	/note="Epitope in FG loop"
FT	Region	210..218

	/note= "Epitope including C3C4 linker"
FT	Region
FT	212..215
FT	/note= "Linker between domains C3 and C4"
FT	216..317
Domain	/note= "Igf heavy chain C4 domain"
PV	
PN	WO200220038-AZ.
XX	
PD	14-MAR-2002.
XX	
PF	06-SEP-2001; 2001WO-DK00579.
PR	06-SEP-2000; 2000DK-0001326.
PR	15-SEP-2000; 2000UD-232831P.
PA	(PHAR-) PHARMEXA AS.
PI	Klysnier S, Von Hoegen P, Voldborg B, Gautam A;
PT	WPI: 2002-383033/41.
PT	
PT	Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
PS	-
Disclosure:	Page 105-106; 15pp; English.
This invention relates to a novel method for inducing an immune response against autoantigenic immunoglobulin E (IGE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autoantigenic IGE in an animal, which is useful for downregulating autoimmune IGE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains used to create the epitopes of the invention.	
SQ	Sequence 323 AA;
Query Match	Best Local Similarity 100.0%; Score 1707; DB 23; Length 323; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY	1 FTTPVTIVILSSCGGCHFPPTIDLLCVSSTPGTINITWLDEGVVDVLASTAQOE 60 Db 4 FTFPTVIILSSCGGGHFFPTIQDLCIVSGTYFETINITWLDEGVVDVLASTAQOE 63 DY 61 GELASTOSELTLSOKHWLSDRTYTCCQVLYTGHTFEEDSTRKCADSNRGVSAYLSRSPFD 120 Db 64 GELASTOSELTLSOKHWLSDRTYTCCQVLYTGHTFEEDSTRKCADSNRGVSAYLSRSPFD 123 DY 121 LFIKKSTPTICLVVDLPASRKCTVALWTMSRAKGKVNHSTREEKEORNGTLTVISTLPYGVT 180 Db 124 LFIRKSPTITCLVVLDLPASKGTVAULTWSRASGPVNHNSTRKEEKORNGLTVTSTLPVGTT 183 DY 181 RDWIIEGETTCRVNHPHLPRALMNSTKTSCPPRAPAEVYAFAPEMPGSRRKRFLACLIQ 240 Db 184 RDMTEGETYCQRVTHPHPLRALMNSTTKTSPPRAAPEVIAATATEWPGRSRKRFLACLIQ 243 OY 241 NFMEDISVOVLHNEVOLDPDAHSSTOPRKTKSGGFVFESRLLEVRTAAEMWKDFEICRAY 300 DB 244 NFMEDEDISOVLHNEVOLDPDAHSHSTOPRKTKSGGFVFESRLLEVRTAAEMWKDFEICRAY 303 OY 301 HEAASPQTQQRAVSVPNGK 320 DB 304 HEAASPQTQQRAVSVPNGK 323

XX	AAU80285 standard; Protein: 323 AA.
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AC	AAU80285;
XX	
DT	30-JUL-2002 (first entry)
XX	
DE	Human Ige C2-C3-C4 domains for mammalian expression.
KW	Ige: allergy; human; antiallergic; immunosuppressive; antiaphyllactic;
KM	antisthmatic; dermatological; antiinflammatory; immunoglobulin E; Ige;
KW	vaccine; anaphylaxis; allergic rhinitis; asthma; atopc dermatitis;
KW	heavy chain C domain.
XX	
OS	Homo sapiens.
OS	Synthetic.
PN	WO200220038-A2.
XX	
PD	14-MAR-2002.
XX	
PF	06-SEP-2001; 2001WO-DK00579.
XX	
PR	06-SEP-2000; 2000DK-0001326.
PR	15-SEP-2000; 2000US-232831P.
XX	
PA	(PHAR-) PHARMEXA AS.
XX	
PI	Klysnar S, Von Hoejen P, Voldborg B, Gautam A;
DR	WPI: 2002-383033/41.
DR	N-PSDB: ABK51133.
PT	
PT	Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
XX	
PS	Disclosure; Page 108-110; 151pp; English.
CC	This invention relates to a novel method for inducing an immune response
CC	against autologous immunoglobulin E (Ige) in an animal. The method
CC	comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC	(CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
CC	epitope (TH epitope) which is foreign to the animal, by antigen
CC	presenting cells (APCs) of the animal's immune system. The epitopes
CC	of the invention may be used as a vaccine against allergic diseases. The
CC	method of the invention is useful for inducing an immune response
CC	against autologous Ige in an animal, which is useful for downregulating
CC	autologous Ige in the animal. This method is useful in the prevention
CC	and treatment of allergic diseases such as anaphylaxis, allergic
CC	rinitis, asthma and atopc dermatitis. The present sequence represents
CC	the human Ige heavy chain C2-C3-C4 domains optimised for expression in a
CC	mammalian system, this sequence was used to create the epitopes of the
CC	invention.
SO	
Sequence	323 AA:
Query Match	100.0%; Score 1707; DB 23; Length 323;
Best Local Similarity	100.0%; Pred. No. 1,1e-129;
Matches 320; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 FPPPYKIIIOSSODGGGHPPTIOLLCVSGTPTNTITMLEGOVDNDLSTASTOE 60
Db	4 FPPPYKIIIOSSODGGGHPPTIOLLCVSGTPTNTITMLEGOVDNDLSTASTOE 63
QY	61 GELASTOSELTISOKHMLSDRYTCOVYTGHTFEEDSTRKCADSNPRGSAYLSRSPFD 120
Db	.64 GELASTOSELTISOKHMLSDRYTCOVYTGHTFEEDSTRKCADSNPRGSAYLSRSPFD 122
QY	121 LFRKSPPTITCLVLWDLPASKGTIVLFWBSAGSKPVNHSSTRKEORNGCTLVTVSTPLPGVT 180

Db 124 LFIKSPITICLVVDLAPSKGVLTWRSAGKPVNSTRKEEKORNGTLTVSTLPGT 183
 QY 181 RDWIEGTYOCRTVTHPHLPALMRSTTKSGPRAPEVYAFAPPEWGSRRKRTLACLIQ 240
 Db 184 RDWIEGTYOCRTVTHPHLPALMRSTTKSGPRAPEVYAFAPPEWGSRRKRTLACLIQ 243
 QY 241 NFMEDISVQMLHNEVOLPDARHSTTPRKTKSGGFVFSRLVETRAEMEQKDEFICRAV 300
 Db 244 NFMEDISVQMLHNEVOLPDARHSTTPRKTKSGGFVFSRLVETRAEMEQKDEFICRAV 303
 QY 301 HEASPSQTVQRAVSVNPGK 320
 Db 304 HEASPSQTVQRAVSVNPGK 323
 RESULT 3
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 ID AA080286 standard; Protein: 323 AA.
 AC AA080286;
 XX
 DT 30-JUL-2002 (first entry)
 DE Human Ige C2-C3-C4 domains for E.Coli expression.
 XX
 KW IGF: allergy; human; antiallergic; immunosuppressive; antianaphylactic;
 antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IGF;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 heavy chain C domain.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX
 PN W0200220038-A2.
 PD 14-MAR-2002.
 PE 06-SEP-2001; 2001WO-DK00579.
 PR 06-SEP-2000; 2000DK-0001326.
 PR 15-SEP-2000; 2000US-232831P.
 XX
 PA (PHAR-) PHARMEXA AS.
 PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;
 DR WPI: 2002-383033/41.
 DR N-PSDB: ABR51134.
 PT Inducing immune response against autologous immunoglobulin E in an
 animal, by effecting simultaneous presentation of cytotoxic T
 lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
 .
 PT
 XX Disclosure: Page 112-113; 151pp; English.
 XX
 CC This invention relates to a novel method for inducing an immune response
 against autologous immunoglobulin E (Ige) in an animal. The method
 comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
 epitope (TH epitope) which is foreign to the animal, by antigen
 presenting cells (APCs) of the animal's immune system. The epitopes
 of the invention may be used as a vaccine against allergic diseases. The
 method of the invention is useful for inducing an immune response
 against autologous Ige in an animal, which is useful for downregulating
 autologous Ige in the animal. This method is useful in the prevention
 and treatment of allergic diseases such as anaphylaxis, allergic
 rhinitis, asthma and atopic dermatitis. The present sequence represents
 the human Ige heavy chain C2-C3-C4 domains optimised for expression in
 an E. Coli system, this sequence was used to create the epitopes of the
 invention.
 CC
 XX

SQ Sequence 323 AA;
 Query Match 100.0%; Score 1707; DB 23; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1,1e-129;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYPTGTINITWLEDGYMDVLDSTASTTOE 60
 Db 4 FTPTVKILQSSCDGGHFPPTIQLCLVSGYPTGTINITWLEDGYMDVLDSTASTTOE 63
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 Db 64 GELASTOSELTLSCKHMLSDRTTYCOVYTGHTFEDSTKCCADSNPGVSATYLSRSPFD 123
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 Db 124 LFIKSPITICLVVDLAPSKGVLTWRSAGKPVNSTRKEEKORNGTLTVSTLPGT 183
 QY 181 RDWIEGTYOCRTVTHPHLPALMRSTTKSGPRAPEVYAFAPPEWGSRRKRTLACLIQ 240
 Db 184 RDWIEGTYOCRTVTHPHLPALMRSTTKSGPRAPEVYAFAPPEWGSRRKRTLACLIQ 243
 QY 241 NFMEDISVQMLHNEVOLPDARHSTTPRKTKSGGFVFSRLVETRAEMEQKDEFICRAV 300
 Db 244 NFMEDISVQMLHNEVOLPDARHSTTPRKTKSGGFVFSRLVETRAEMEQKDEFICRAV 303
 QY 301 HEASPSQTVQRAVSVNPGK 320
 Db 304 HEASPSQTVQRAVSVNPGK 323
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 AC AAR83559;
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 DT 06-MAR-1996 (first entry)
 DE Fc(epsilon)-CH2'-CH4' protein-sequence.
 XX
 KW Fc(epsilon); antibody; human; myeloma; probe; Ige; tryptophan promoter;
 KW constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
 KW histamine; anti-allergenic; vaccine; immune response.
 KW
 XX Synthetic.
 OS
 PN FR2715304-A1;
 PD 28-JUL-1995.
 PE 26-JAN-1994; 94FR-0000846.
 PR 26-JAN-1994; 94FR-0000846.
 PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS.
 PI Hurpin CM, Panero MJM;
 DR WPI: 1995-265243/35.
 DR N-PSDB: AAT01865.
 PT Antiallergic vaccine contg. polypeptide fragment of Ige heavy chain
 PT - has epitope(s) not present in native Ige, also derived antibodies
 PT for treating or preventing allergies, inflammatory immune disease,
 PT etc.
 XX Claim 3; Page 32-33; 44pp; French.
 PS The amino acid sequence of the Fc(epsilon) CH2'-CH4' fragment covering
 CC amino acids 226-547. The DNA sequence was isolated from a human myeloma
 CC 266BL CDNA library screened with a probe corresp. to the N-terminus of
 CC Ige. The region encoding amino acids 218-547 was cloned into the vector
 CC
 XX

CC pwt211 under control of the tryptophan promoter. The resultant protein
 CC produced contains some non-Fc amino acids. These were removed by
 CC replacing their coding sequence with a bicistronic linker. The resultant
 CC construct encodes the Fc(epsilon) constant heavy region from amino acids
 CC 226-547. When it is expressed in E.coli, the protein produced is a
 CC non-glycosylated Fc(epsilon) fragment. Altering the pattern of
 CC glycosylation unmasks new antigenic sites thus rendering the Fc fragment
 CC immunogenic and able to induce antibodies that recognise native IgE but
 CC do not form histamine-releasing complexes. The Fc fragments can be used
 CC in anti-allergic vaccines to modulate the intensity of immune responses
 CC mediated by IgE.

XX Sequence 324 AA;

Query Match 100.0%; Score 1707; DB 16; Length 324;

Best Local Similarity 100.0%; Pred. No. 1.1e-129;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCGGHPPTIQLCLVSGYPTGTINITWLEDQVMDVLDLSTASTOE 60
 DB 5 FTPTVKILQSSCGGHPPTIQLCLVSGYPTGTINITWLEDQVMDVLDLSTASTOE 64
 QY 61 GELASTOSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 120
 DB 65 GELASTOSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 124
 QY 121 LFIKSPITICLVVDLAPSKGTVNLMTWSRASGKPVNHSRKEEKORNGTLTVSTLPVGT 180
 DB 125 LFIKSPITICLVVDLAPSKGTVNLMTWSRASGKPVNHSRKEEKORNGTLTVSTLPVGT 184
 QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 240
 DB 185 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 244
 QY 241 NFMEDISVQMLHNEVQLPARHSTTOPRKTGSGFEVFSRLLEVTRAEMEQKDEFTICRAV 300
 DB 245 NFMEDISVQMLHNEVQLPARHSTTOPRKTGSGFEVFSRLLEVTRAEMEQKDEFTICRAV 304
 QY 301 HEAAPSQTVQRAVSVPNGK 320
 DB 305 HEAAPSQTVQRAVSVPNGK 324

RESULT 5

AAR75225 standard; Protein: 325 AA.

XX AAR75225;

XX 10-NOV-1995 (first entry)

XX Human IgE Fc chain (amino acids 224-547) mutant sequence.

XX IgE Fc fragment; antiallergic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 148 /label= Asn371

FT Misc-difference 172 /note= "glycosylation site"

FT Misc-difference 172 /label= Asn394

FT Misc-difference 1 /note= "glycosylation site"

FT Misc-difference 1 /label= Val224

FT Misc-difference 2 /note= "any AA or deletion"

FT Misc-difference 3 /note= "Ala, any other AA, or deletion"

FT Misc-difference 3 /label= Ser226

FT /note= "any AA or deletion"

FT Misc-difference 4 /label= Arg227
 FT /note= "any AA or deletion"
 FT Misc-difference 5 /label= Asp228
 FT /note= "any AA or deletion"

PN W09514779-A.

XX 01-JUN-1995.

XX 22-NOV-1994; 94WO-CB02561.

XX 22-NOV-1993; 93GB-0024013.

XX (THRE-) 31 RES EXPL LTD.

XX (CLT) CELLTECH THERAPEUTICS LTD.

XX Gould HJ, Owens RJ, Sutton BJ, Young RJ;

XX WPI: 1995-206936/27.

XX DR NPSDB: AA087474.

XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc

XX useful to study and treat allergy.

XX Disclosure; Page 6; 55pp; English.

XX The sequence represents a mutant sequence of a human IgE-Fc.

XX chimeric amino acids 224-547, which is of sufficient length to bind

XX Fc-epsilon RI and/or Fc-epsilon RI IgE receptor sites on human

XX cells. The protein is useful in the study and treatment of

XX allergy.

XX Sequence 325 AA;

XX Query Match 100.0%; Score 1707; DB 16; Length 325;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-129;

XX Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCGGHPPTIQLCLVSGYPTGTINITWLEDQVMDVLDLSTASTOE 60

DB 6 FTPTVKILQSSCGGHPPTIQLCLVSGYPTGTINITWLEDQVMDVLDLSTASTOE 65

QY 61 GELASTOSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 120

DB 66 GELASTOSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 125

QY 121 LFIKSPITICLVVDLAPSKGTVNLMTWSRASGKPVNHSRKEEKORNGTLTVSTLPVGT 180

DB 126 LFIKSPITICLVVDLAPSKGTVNLMTWSRASGKPVNHSRKEEKORNGTLTVSTLPVGT 185

QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 240

DB 186 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 245

QY 241 NFMEDISVQMLHNEVQLPARHSTTOPRKTGSGFEVFSRLLEVTRAEMEQKDEFTICRAV 300

DB 246 NFMEDISVQMLHNEVQLPARHSTTOPRKTGSGFEVFSRLLEVTRAEMEQKDEFTICRAV 305

QY 301 HEAAPSQTVQRAVSVPNGK 320

DB 306 HEAAPSQTVQRAVSVPNGK 325

RESULT 6

AAR77241 standard; Protein: 325 AA.

XX AAR77241;

XX 10-NOV-1995 (first entry)

Query Match	100.0%	Score 1707	DB 16	Length 325
Best Local Similarity	100.0%	Pred. No. 1.1e-129		
Matches 320	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	FTPTPTVVLIISSDCGGHPRPTIOLCLVSGYPTGTTINIMWLEGGQVMDVDSLSTAOE	60	
DB	6	FTPTPTVVLIISSDCGGHPRPTIOLCLVSGYPTGTTINIMWLEGGQVMDVDSLSTAOE	65	
QY	61	GELASTQSELTLSQKHWLSDRTYTCQVYTGQHPEDSTKKCADSNPRGVSAYLSRSPFD	120	
DB	66	GELASTQSELTLSQKHWLSDRTYTCQVYTGQHPEDSTKKCADSNPRGVSAYLSRSPFD	125	
QY	121	LFTKSPPTICLVVDLAPSKGTWNLWMSRASGKPVNHSSTRKEEKORNGTLTVSTLPVGT	180	
DB	126	LFTKSPPTICLVVDLAPSKGTWNLWMSRASGKPVNHSSTRKEEKORNGTLTVSTLPVGT	185	
QY	181	RDWTEGSETTCORVTHPLPRALMSTKTKSGPRAPRVYAFAPTEWPGSGSDKRTLACLIQ	240	
DB	186	RDWTEGSETTCORVTHPLPRALMSTKTKSGPRAPRVYAFAPTEWPGSGSDKRTLACLIQ	245	
QY	241	NFMPEDEISVOMLHNEVOLDPARHSTQPRKTKSGGFVFSRLLEVTRAEMEQKDEFICRAV	300	
DB	246	NFMPEDEISVOMLHNEVOLDPARHSTQPRKTKSGGFVFSRLLEVTRAEMEQKDEFICRAV	305	
QY	301	HEAASPSQTYVORAVSNVPGK 320		
DB	306	HEAASPSQTYVORAVSNVPGK 325		

RESULT	7
AAB03642	ID AAB03642 standard; protein: 331 AA.
XX	AC AAB03642;
XX	DT 22-NOV-2000 (first entry)
XX	DE Human IgE heavy chain constant regions 2, 3 and 4.
XX	KW Human; immunoglobulin E; IgE; vaccination; infection; allergy;
XX	KW asthma; eczema; immunogenic peptide.
OS	Homo sapiens.
PN	MO200025722-A2.
PD	11-MAY-2000.
PF	21-OCT-1999; 99WO-SE01896.
PR	02-NOV-1998; 98US-010652.
PR	22-SEP-1999; 99US-0401636.
PA	(RESI-) RESISTENTIA PHARM AB.
P1	Heilman LT;
DR	WPI: 2000-365342/31.
XX	Immunogenic polypeptides useful for preventing the harmful effects of
PT	immunoglobulin E in mammals
PS	Disclosure: Fig 1; 50pp; English.
XX	The present sequence is an immunogenic peptide consisting of the
CC	heavy chain constant regions 2, 3 and 4 of the human IgE. It was used to
CC	construct a number of immunogenic peptides which consisted of regions of
CC	IgE from different mammals, which appear to cause a stronger polyclonal
CC	anti-self IgE response than peptides consisting of the same regions from
CC	one mammal. Immunogenic peptides, particularly those consisting of
CC	different heavy chain constant regions, can be used for vaccination
CC	in humans, against bacterial and viral infections and allergies, such
CC	as asthma, fur, pollen and food allergies and eczema.
XX	Sequence 331 AA:
SQ	Query Match 100.0%; Score 1707; DB 21; Length 331;
	Best Local Similarity 100.0%; Pred. No. 1.1e-129;
	Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 FTPTVKILGSSCDGGHFPPTIOLLCLVSGYTPGTINITWLDEGVMDVLSTASTQE 60
DB	
	12 FTPTVKILGSSCDGGHFPPTIOLCLVSGYTPGTINITWLDEGVMDVLSTASTQE 71
OY	61 GELASTOSELTLSQKHWISDRTYTCQVYYOGHTFEDSKKKCADSNPBGVSATLSPSPD 120
DB	
	72 GELASTOSELTLSQKHWISDRTYTCQVYYOGHTFEDSKKKCADSNPBGVSATLSPSPD 131
OY	121 LFIKRSPTITLVLDLAPASKGTIVNLTWGRASGKPVNHSSTRKEKORNGTLVTSTLPVGT 180
DB	
	132 LFIRKSPTITLVLDLAPASKGTIVNLTWGRASGKPVNHSSTRKEKORNGTLVTSTLPVGT 191
OY	181 RDMIEGETYQCRVTHPHLPRLALMSTTTSQGPRAAEVYAFAETPEWPGSRDKRTLACLIO 240
DB	
	192 RDWIEGETYQCRVTHPHLPRLALMSTTTSQGPRAAEVYAFAETPEWPGSRDKRTLACLIO 251
OY	241 NFMFEDSISVQMLHNENVOGLDARHSTTORPKTKGSSEFFVSRLEVTYRAAMEOKDEFICAV 300
DB	NFMFEDSISVQMLHNENVOGLDARHSTTORPKTKGSSEFFVSRLEVTYRAAMEOKDEFICAV 311
OY	301 HEAASPQTQRAVASVPNGK 320

[illegible]

Oy		241	NFMPEDISVOMLNEVQLPDARHSTTOPRKTGSGFPWFESRLLEYTRAMEOKDEICRAV	3000
Dd		288	NFMPEDISVOMLNEVQLPDARHSTTOPRKTGSGFPWFESRLLEYTRAMEOKDEICRAV	3477
OY		301	HEAASPSQTFVORAVSVNPGK	320
Db		348	HEAASPSQTFVORAVSVNPGK	367
RESULT	9			
ID	AAU80283			
XX	AAU80283	standard; Protein; 428 AA.		
AC	AAU80283;			
XX				
DT	30-JUL-2002	(first entry)		
De				
XX				
KW	Human IgE heavy chain C1-C2-C3-C4 domains.			
KW	IgE: allergy; human; antiallergic; immunosuppressive; antiaphyllactic;			
KW	antihistaminic; dermatological; antiflammatory; immunoglobulin E; IgE;			
KW	vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;			
KW	heavy chain C domain.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	Domain	11..116	/note= "IgE heavy chain C1 domain"	
FT	Domain	113..208	/label= "IgE heavy chain C2 domain"	
FT	Region	205..219	/note= "Epitope including C2C3 linker"	
FT	Region	209..216	/note= "Linker domain between C2 and C3 region"	
FT	Domain	217..316	/note= "IgE heavy chain C3 domain"	
FT	Region	244..251	/note= "Epitope in BC loop"	
FT	Region	244..251	/note= "Epitope in BC loop"	
FT	Region	244..251	/note= "Epitope in DE loop"	
FT	Region	301..311	/note= "Epitope in FG loop"	
FT	Region	315..323	/note= "Epitope including C3C4 linker"	
FT	Region	317..320	/note= "Linker between domains C3`andC4"	
FT	Domain	321..422	/note= "IgE heavy chain C4 domain"	
PN	WO200220038-A2.			
PD	14-MAR-2002.			
PE	06-SEP-2001; 2001WO-DK0579.			
PR	06-SEP-2000; 2000DK-0001326.			
PA	15-SEP-2000; 2000US-232831P.			
PHAR-	PHARMEXA AS.			
Pt	Klysner S, Von Hoegen P, Voldborg B, Gautam A;			
WI:	2002-383033/41.			
PT	Inducing immune response against autologous immunoglobulin E in an			
PT	animal, by effecting simultaneous presentation of cytotoxic T			
PT	lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin			

Db 409 HEASPSQTVORAVSVNPGK 428

RESULT 11
 ID AAM47863 standard; Protein: 428 AA.
 AC AAM47863;
 DT 22-FEB-2002 (first entry)
 DE Human Ig-E heavy chain constant region amino acid sequence.
 KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 KW transgenic plant.
 OS Homo sapiens.
 PN WO200183529-A2.
 PD 08-NOV-2001.
 PF 28-APR-2001; 2001WO-US13932.
 PR 28-APR-2000; 2000US-200298P.
 PA (PLAN-) PLANET BIOTECHNOLOGY INC.
 PI Larick JW, Wycoff KL;
 DR WPI: 2002-041481/05.
 DR N-PSDB; ABA052278.
 PT Immunoadhesin for treating human rhinovirus infection comprises
 PT chimeric intercellular adhesion molecule-1, and optionally a J chain
 PT and secretory component in association -
 PS Disclosure: Fig 7; 138pp; English.

The invention relates to an immunoadhesin comprising:
 (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a
 rhinovirus receptor protein linked to at least a portion of an
 immunoglobulin heavy chain; and
 (b) optionally a J chain and secretory component associated with the
 chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
 glycosylation and virucide activity. The immunoadhesin is useful for
 reducing infection and human rhinovirus (HRV) and hence the initiation or
 spread of the common cold by HRV. The immunoadhesin binds to HRV and
 reduces its infectivity, competing with cell surface ICAM-1 for binding
 sites, interfering with virus entry or uncoating and directing premature
 release of viral RNA and formation of empty capsids. Expression of the
 immunoadhesin in plants would be tetrameric, rather than dimeric.
 Immunoadhesin having multiple binding sites have a higher effective
 affinity for the virus, thereby increasing the effectiveness of the
 immunoadhesin. Association of secretory component and immunoglobulin J
 chain increases the stability of the immunoadhesin in the mucosal
 environment. Production is significantly less expensive in plants than in
 animal cell culture and production in plants is safer for human use,
 since plants are not known to harbor any animal viruses. The present
 sequence is that of a human immunoglobulin protein sequence, useful to
 the invention.

Query Match 100.0%; Score 1707; DB 23; Length 428;
 Best Local Similarity 100.0%; Pred. No. 1,5e-129;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FTPTPTVKILQSSCGSGGHFPPTIQLLIVSGYPTGTINITWLEDGQVMDVLSASTTQOE 60
 109 FTPTPTVKILQSSCGSGGHFPPTIQLLIVSGYPTGTINITWLEDGQVMDVLSASTTQOE 168

QY 61 GELASTOSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCADSNPRGVSAVLSRSPFD 120
 Db 169 GELASTOSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCADSNPRGVSAVLSRSPFD 228
 QY 121 LFIKRSPTITCLVVDLAPSKCTVNLWTSRAGKRVNHSRKEEQQRNLTLLVSTLPVGT 180
 Db 229 LFIKRSPTITCLVVDLAPSKCTVNLWTSRAGKRVNHSRKEEQQRNLTLLVSTLPVGT 288
 QY 181 RDWIEGETYQCRVTHPHLPALMRSTKTSQGPRAPEVYAFATPEMPGSRDKRTLACLIQ 240
 Db 289 RDWIEGETYQCRVTHPHLPALMRSTKTSQGPRAPEVYAFATPEMPGSRDKRTLACLIQ 348
 QY 241 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSKLEVTYRAEMQKDEFICRAV 300
 Db 349 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSKLEVTYRAEMQKDEFICRAV 408
 QY 301 HEASPSQTVORAVSVNPGK 320
 Db 409 HEASPSQTVORAVSVNPGK 428

RESULT 12
 ID AAY79994 standard; Protein: 325 AA.
 AC AAY79994;
 DT 15-MAY-2000 (first entry)
 DE Human immunoglobulin E epsilon heavy chain SEQ ID NO:1.
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 OS Homo sapiens.
 PN WO9967293-A1.
 PD 29-DEC-1999.
 PF 21-JUN-1999; 99WO-US13959.
 PR 20-JUN-1998; 98US-0100287.
 PA (UNBI-) UNITED BIOMEDICAL INC.
 PI Wang CY, Walfield AM;
 DR WPI: 2000-160578/14.
 PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy -
 PS Example 1; Page 66-68; 155pp; English.

The present invention describes immunoglobulin E (IgE)-CH3 domain
 antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
 and anti-asthmatic properties. (I) induces polyclonal antibodies
 specific for a target effector site on the epsilon-heavy chain of IgE,
 and so preventing triggering and activation of mast cells and basophils
 CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe
 CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino

CC acid sequences used in the exemplification of the present invention.

XX Sequence 325 AA:

Query Match 99.6%; Score 1701; DB 21; Length 325;

Best Local Similarity 99.4%; Pred. No. 3.3e-129;

Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 FTPTVVKILQSSCDGGHPPPTIQLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQ 60
   |||
DB 6 FTPTVVKILQSSCDGGHPPPTIQLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQ 65
   |||
QY 61 GELASTQSELTLSQKHWLSDRTTYCOVYQGHTEFEDSTKCKADSNPRGSAVLSRSP 120
   |||
DB 66 GELASTQSELTLSQKHWLSDRTTYCOVYQGHTEFEDSTKCKADSNPRGSAVLSRSP 125
   |||
QY 121 LFIKRSPTITCLVLDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLVTSLLPVGT 180
   |||
DB 126 LFIKRSPTITCLVLDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLVTSLLPVGT 185
   |||
QY 181 RDMWIGETYQCRVTHPHLPALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 240
   |||
DB 186 RDMWIGETYQCRVTHPHLPALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 245
   |||
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFEVFSRLVETRAEWEQKDEFICRAV 300
   |||
DB 246 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFEVFSRLVETRAEWEQKDEFICRAV 305
   |||
QY 301 HEAASPSQTVQRAVSNP 320
   |||
DB 306 HEAASPSQTVQRAVSNP 325
   |||
```

RESULT 13

AAU80288 standard; Protein; 336 AA.

AC AAU80288;

DT 30-JUL-2002 (first entry)

DE Human IGE heavy chain C2-C3-C4 domains with MIGIS fragment.

XX IGE; allergy; human; antiallergic; immunosuppressive; anti-anaphylactic;

KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IGE;

KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;

KW heavy chain C domain; MIGIS.

OS Homo sapiens.

OS Synthetic.

XX

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XX

XX

XX

FT Domain /note= "IGE heavy chain C3 domain"

FT 322..336

FT /note= "MIGIS fragment"

PN WO200220038-A2.

PD 14-MAR-2002.

PF 06-SEP-2001; 2001WO-DK00579.

PR 06-SEP-2000; 2000DK-0001326.

PR 15-SEP-2000; 2000US-232831P.

PA (PHAR-) PHARMEXA AS.

PI Klysnen S, Von Hoegen P, Voldborg B, Gautam A;

DR WPI; 2002-383033/41.

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Examples: Page 116-117; 151pp; English.

This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IGE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IGE in an animal, which is useful for downregulating CC autologous IGE in the animal. This method is useful in the prevention CC and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents CC the human IGE heavy chain C2-C3-C4 domains fused to the MIGIS CC fragment used to create the epitopes of the invention.

Sequence 336 AA:

Query Match 99.4%; Score 1696; DB 23; Length 336;

Best Local Similarity 100.0%; Pred. No. 8.6e-129;

Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 FTPTVVKILQSSCDGGHPPPTIQLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQ 60
   |||
DB 4 FTPTVVKILQSSCDGGHPPPTIQLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQ 63
   |||
QY 61 GELASTQSELTLSQKHWLSDRTTYCOVYQGHTEFEDSTKCKADSNPRGSAVLSRSP 120
   |||
DB 64 GELASTQSELTLSQKHWLSDRTTYCOVYQGHTEFEDSTKCKADSNPRGSAVLSRSP 123
   |||
QY 121 LFIKRSPTITCLVLDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLVTSLLPVGT 180
   |||
DB 124 LFIKRSPTITCLVLDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLVTSLLPVGT 183
   |||
QY 181 RDMWIGETYQCRVTHPHLPALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 240
   |||
DB 184 RDMWIGETYQCRVTHPHLPALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 243
   |||
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFEVFSRLVETRAEWEQKDEFICRAV 300
   |||
DB 244 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFEVFSRLVETRAEWEQKDEFICRAV 303
   |||
QY 301 HEAASPSQTVQRAVSNP 318
   |||
DB 304 HEAASPSQTVQRAVSNP 321
   |||
```

RESULT 14

AAU80287	standard; Protein; 441 AA.
AAU80287	
30-JUL-2002	(first entry)
Human IGE heavy chain C1-C2-C3-C4 domains with MIGIS fragment.	
IGF: allergic; human; antiallergic; immunosuppressive; antianaphylactic;	
antihistaminic; dermatologic; antiinflammatory; immunoglobulin E; IGE;	
vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;	
heavy chain C domain; MIGIS.	
Homo sapiens.	
Synthetic.	
Location/Qualifiers	
11..106	/note="IGE heavy chain C1 domain"
113..208	/label="IGE heavy chain C2 domain"
205..219	/note="Epitope including C2C3 linker"
209..216	/note="Linker domain between C2 and C3 region"
217..317	/note="IGE heavy chain C3 domain"
244..251	/note="Epitope in BC loop"
244..251	/note="Epitope in BC loop"
244..251	/note="Epitope in BC loop"
272..280	/note="Epitope in DE loop"
301..311	/note="Epitope in FG loop"
315..323	/note="Epitope including C3C4 linker"
318..320	/note="Linker between domains C3 and C4"
321..422	/note="IGE heavy chain C4 domain"
427..421	/note="MIGIS fragment"
MO200220038-A2.	
14-MAR-2002.	
06-SEP-2001; 2001WO-DK00579.	
06-SEP-2000; 2000DK-0001376.	
15-SEP-2000; 2000US-232831P.	
(PHAR-) PHARMEXA AS.	
Klynsner S, Von Hoegen P, Voldborg B, Gautam A;	
WPI; 2002-383033/41.	
Inducing immune response against autologous immunoglobulin E in an	
animal, by effecting simultaneous presentation of cytotoxic T	
lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin	
Examples: Page 116-117; 151pp; English.	
This invention relates to a novel method for inducing an immune response	
against autologous immunoglobulin E (IGE) in an animal. The method	
comprises effecting simultaneous presentation of cytotoxic T lymphocyte	
(CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell	
epitope (TH epitope) which is foreign to the animal, by antigen	
presenting cells (APCs) of the animal's immune system. The epitopes	

	CC	of the invention may be used as a vaccine against allergic diseases. The
	CC	method of the invention is useful for inducing an immune response
	CC	against autologous IgE in an animal, which is useful for downregulating
	CC	autologous IgE in the animal. This method is useful in the prevention
	CC	and treatment of allergic diseases such as anaphylaxis, allergic
	CC	rhinitis, asthma and atopic dermatitis. The present sequence represents
	CC	the human IgE heavy chain C1-C2-C3-C4 domains fused to the MIGIS
	CC	fragment used to create the epitopes of the invention.
XX	Sequence	441 AA;
SO	Query Match	99.4%; Score 1696; DB 23; Length 441;
	Best Local Similarity	100.0%; Pred. No. 1,2e-128;
	Matches 318:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	I FTPPTVKRILSSCGGGHFPPTIDLLCVSGYTGTINITWLEDSQVMDVDLSTASTOE	60
Dd	109 FTTPTVKRILOSSCDGGEHPPTIOLLCVSGTPEETINITWLEDQVMDVDLSTASTQE	168
OY	61 GELASTOSELTLSOKHMLSDRTYTCQVLYQGHTFEDSTKKCADSNPRGSAYLSRPSPD	120
Dd	169 GELASTOSELTLSQKHMLSDRITYTCQVLYQHTEFDSTKKCADSNPRGSAYLSRPSPD	228
OY	121 LFIKRSPIITLVVDLAPSKGTIVNLTWRASAGKPVNHSTRKEEKORNTLYVTSLPYGT	180
Dd	229 LFIRKSPIITCLVVDLAPSKGTIVNLTWSRASGPVNHSRKEEKORNTLYVTSLPYGT	288
OY	181 RDWIEGETYOCRAVTHPHLPRLALMRSTYKTSGPRAPEVYAATPEMPGSRDKRTLACLIQ	240
Dd	289 RDMIEGETYOCRAVTHPHLPRLALMSTYKTSGPRAPEVYAATPEMPGSRDKRTLACLIQ	348
OY	241 NFMPEDISVOMLHNEDVQLPDARHSTTOPRKTKSGFEVFYSRLRYTRAEMQKDEFICRAY	300
Dd	349 NFMPEDISVOMLHNEDVQLPDARHSTTOPRKTKSGFEVFYSRLRYTRAEMQKDEFICRAY	408
OY	301 HEAASPQSOTVORAHSVNP 318	
Dd	409 HEAASPQSOTVORAHSVNP 426	
	RESULT 15	
	AAP40065	
ID	AAP40065 standard; Protein: 493 AA.	
XX	AA40065;	
XX	12-FEB-1992 (first entry)	
DE	Sequence of human immunoglobulin E H-chain.	
KW	Antibody; allergy suppressor; immunological.	
OS	Homo sapiens.	
PN	EPI02634-A.	
PD	14-MAR-1984.	
PF	03-SEP-1983; 83EP-0108699.	
PR	07-SEP-1982; 82JP-0156285.	
PA	(TAKE) TAKEDA CHEMICAL IND KK.	
PI	Kikuchi M., Kurokawa T., Onda H;	
DR	WPI: 1984-070437/12.	
DR	N-PSDB; AAM40062.	
PT	Polypeptide having activity of human immunoglobulin E - prepd.	
PT	from host transformed with recombinant DNA	
SS	Disclosure; Fig 2; 6lpp: English.	

XX DNA encoding Ige H-chain and frags. is claimed (AAN40062).
CC Transformant contg. the DNA is also new, esp. Escherichia coli IFO-
CC 14284, -5 and -6. The transformant may be grown to produce a
CC polypeptide of immunological or biological activity equivalent to
CC that of the human Ige H chain. AAN40062 or frags. is pref. linked at a
CC site downstream from a promoter, e.g. rec A promoter (see AAN40064).
XX

SQ Sequence 493 AA:

Query Match 99.2%; Score 1693; DB 5; Length 493;
Best Local Similarity 99.4%; Pred. No. 2.5e-128;

Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	FTPTVKILQSSCDGSGHFPPTIOLCLVSGYTPCTINITWLEDGQVMDVDLSTASTOE	60
DB	174	FTPTVKILQSSCDGSGHFPPTIOLCLVSGYTPCTINITWLEDGQVMDVDLSTASTOE	233
QY	61	GELASTQSELTLISQKHWLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAVLSRSPED	120
DB	234	GELASTQSELTLISQKHWLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAVLSRSPED	293
QY	121	LFIRKSPITTCIVVDLAPSKGTVNLTWSRASGKPVNHSTRKEKORNGTLVTSFLPVGT	180
DB	294	LFIRKSPITTCIVVDLAPSKGTVNLTWSRASGKPVNHSTRKEKORNGTLVTSFLPVGT	353
QY	181	RDWIGETVQCVRPHLPALMRSTKTSGRAPAEVYAFATPEMPSGRDRTLACLIO	240
DB	354	RDWIGETVQCVRPHLPALMRSTKTSGRAPAEVYAFATPEMPSGRDRTLACLIO	413
QY	241	NMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFVFSRLVTRAEMEQRDEFICRAV	300
DB	414	NMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFVFSRLVTRAEMEQRDEFICRAV	473
QY	301	HEAASPSQTVQRAVSVNPGK	320
DB	474	HEAASPSQTVQRAVSVNPGK	493

Search completed: July 15, 2003, 06:57:40
Job time : 39.6806 secs

Db 4 TAPKVFALAPGC--GTTSDSTVALGCLVSGYFEPKVKSW--NSGSLTSGVHTFSPVLQSS 60
QY 62 ELASTOSELTLSQKHMISDRITTYCQVYQGHTE-----DSTKKCADSN--PR--- 107
Db 61 GFYSLSWVYVPAWSTSE--TYICNVVHAASNFVKYKRIEPIPDNHQVCKMSKPCPA 119
QY 108 -----GVSAYLSRSPSPD-LFIRKSPITTCVLDVLAWSKGVNLJWSASAKPYNHNRK 161
Db 120 PELLGGFSPVFLEPPNPMDTLITRTPEVTCVVDVSOENPDVKFNWYDGVETATTRP 179
QY 162 EKKRNGTLVATSTLPGVTRDMIGETVYOCRVTHPHLPALMRSTTSGPRAAEPYAF 221
Db 180 KEQGFNSTYRVSVYLRIOHQMWSKEFKCKVNNQALPQLEIRITTKKSGQSPQYVL 239
QY 222 ATPWPSRDKRTIACLIONMPEDISVQMLHNEVOLPDARHSTTOPRKTGSGFFVFSR 281
Db 240 APHDELKSKSVSTYLVKDFEYPPLEINEMOSNGQPELETXYSTTQAOODSDGSEFYYSK 299
QY 282 LEVTRAEMOEKDEFICRAVHEAASPSQTVORAVSVNPGK 320
Db 300 LSVDRNRMOGCTTTCGVMEHALHNHYT--QANVSKNPGK 337

RESULT 2

ID 08VCX7 PRELIMINARY; PRT; 613 AA.
AC 08VCX7;
DT 01-MAR-2002 (Tremblrel, 20, Created)
DT 01-MAR-2002 (Tremblrel, 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel, 21, Last annotation update)
DE Hypothetical 67.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary Gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC018315; AAI18315.1;
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_5.
DR SMART: SM00409; Ig_2.
DR SMART: SM00407; IgC1; 4.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 25.2%; Score 430.5; DB 11; Length 613;
Best Local Similarity 32.3%; Pred. No. 1e-30;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTYKIIQSSDGC-GGHPPTIQLCLVSGYTPGTINTMLEDGQVMDVLDSTASTQEGE 62
Db 249 PNWNVFVPPRDGSGPAPKRSKLICENTNTPKPTIYVSWLKDGLVSGEFTTPVLTENK 308
QY 63 LASTQ-----SELTLSQKHMISDRITTYCQVYQGHTE-EDSTKKCADSNRGVSAVLSRP 116
Db 309 GSTRPQYKIVSTLTLISIDMLNINVTYCRVDHGLFTLKNVSSGCAASPSDITITPFP 368
QY 117 SPDLPLRKSPTTCLVLDVLAWSKGVNLJWSASAKPYNHNRK 176
Db 369 SFADIFLSKSNLTCLVSNLTAYE-FLNISMASQSGEPLTKIKIMESHNGTFSAGVA 427
QY 177 PVGTROMIEGETVYOCRVTHPHLPALMRSTTSGPRAAEPYAFATP--EWGSGDKRT 234
Db 428 SVCVEEDMNNRKEFVCTVTHRLDPSPOKFLSKNEVHKHPAVAYLLPPAREQLNRESAT 487

QY 235 LACLIONMPEDISVQMLHNEVOLPDARHSTTOPRKTGSG-FFVFSRLVETRAEMQ 292
Db 488 VTCLVKGFSPADISVQMLQRCQLLPQEKYVTSAPMPEGAGFYFTSHILVTEEWNSG 547
QY 293 DEFICRAVHEAASPSQTVORAV 314
Db 548 EFTYCVGHEAL-PLYTERIV 568

RESULT 3

ID 08R3V9 PRELIMINARY; PRT; 469 AA.
AC 08R3V9;
DT 01-JUN-2002 (Tremblrel, 21, Created)
DT 01-JUN-2002 (Tremblrel, 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel, 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC024405; AAI24405.1;
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 24.3%; Score 414; DB 11; Length 469;
Best Local Similarity 29.5%; Pred. No. 2.3e-29;
Matches 97; Conservative 60; Mismatches 154; Indels 18; Gaps 7;

QY 2 TPPTVKIIQSSDGC-GGHPPTIQLCLVSGYTPGTINTMLEDGQVMDVLDSTASTQEG 61
Db 149 TPSPVYPLAPG--SAAQTNSMVTGLCLVKGFEPEPVITW--NSGSLSGVHTFPAVLQSS 204
QY 62 ELASTOSELTLSQKHMISDRITTYCQVYQGHTE-----DSTKKCADSNRGVSAV 112
Db 205 DLYTLSSVTPSPSTWS--QVTCNVNHPASSSTKVDKAIIPROGCKPCICTVPEVSSVF 263
QY 113 LSRSPPD-LFIRKSPITTCVLDVLAWSKGVNLJWSASAKPYNHSTREKQKORNGTLT 171
Db 264 IFFPKRPDVLITITLPRVTCVVDISKDDPEVQSWVDDVENVTAQTKRREQFNSTFR 323
QY 172 VTSLPVGTDMIEGETVYOCRVTHPHLPALMRSTTSGPRAAEPYAFATPPEWGSRD 231
Db 324 SVSELPIMHODWNGKEFKCRVNSAAPPAIEKTIKSKGRPAKPAQVYITIPPEQMAKD 383
QY 232 KRTIACLIONMPEDISVQMLHNEVOLPDARHSTTOPRKTGSGFFVFSRLVETRAEMQ 291
Db 384 KVSILTCMTIDFFPEDITVENQWN--GQPAENYKNTQIPMDTDSYFYSKLNVOKSMWEA 441
QY 292 KDEFCRAVHEAASPSQTVORAVSVNPGK 320
Db 442 GNETFCVLEHGLHNHNT-EKSLSHSPGX 469

RESULT 4

ID 09BSZ1 PRELIMINARY; PRT; 375 AA.
AC 09BSZ1;
DT 01-JUN-2001 (Tremblrel, 17, Created)
DT 01-JUN-2001 (Tremblrel, 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE Hypothetical 41.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;

Query	Database	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	3	24.28	413	375	94	63	159	12	8
Db	32	28.78	29						
QY	63	LA-----	STGBELLSQKHMLSDRTYTCQVYVQGHF	EDSTKKCADSNPKGSAYLSRP	116				
Db	92	ESGPTTKYKVTSTLTIKESDWLSQSMFTCRVDRGLTFQOANSSMCVPPDDTAIRYFAIP	151						
QY	117	SPFDELTKRSPPTICLVVDLAPSKGTVLWTMSRASKGVNNSSTKREKORNGTLTVSTL	176						
Db	152	SFASIFPLKSKTKLCIVYDLT-TYDSVATISWTRONGEAVKTHNTISESHPNATFSAVGEA	210						
QY	177	PVGTRDWTIEGTYOCRTVTHPHLPRLALMRSTTKTSGPRA-ADPVYAF-ATPEWGSRDKRT	234						
Db	211	SICEDDWNSSGRFTCTVYHTDLPSPILKOTISRPKGVALLHRDVTLLPAREQLNRESAT	270						
QY	235	LACIIONMPEDISVOMLHNEVOLDPAHSTTOPR-KTKGSG-FPVFSRLFTTBAEWGQK	292						
Db	271	ITCLVTGSPADVYQWNRQOPLSPREKTYVSAPRPEQAFGRYAHSHILYSEEWNTG	330						
QY	293	DEFCRAVHEAASPSQTVQRAVSVNPGK	320						
Db	331	ETVTCVAHEAL-PNRVTERTVDSKTKG	357						

DR	PROSITE	PS00290; IG_MHC; UNKNOWN.1.
SEQUENCE	463 AA; 51007 MM; EAA674C6BBC30783 CRC64;	
Query Match	24.2%; Score 413; DB 11; Length 463;	
Best Local Similarity	29.2%; Pred. No. 1.8e-29;	
Matches	96; Conservative 61; Mismatches 154; Indels 18; Gaps 7	
OY	2 TPRPYKILQSSCDGGHFPPIIQLCLVSGYTPGIINITWLDGQVMDVLSASTAQEG 61	
Db	143 TPSPSYPLAPG--SAAQTNSMWLTGLCLKGYEPPEVPTVM--NSGSLSSGVTFFPAVLDS 198	
OY	62 ELASQSELTLSQKRWLSDRITYTCQVTVQGHF-----EDSTKKCAQDSNPGVSAV 112	
Db	199 DLYLTSSSVTVPSSTWPSSE-TVTCVNAHPASTKYDKKIVPRDCCPKPTCTVPEVSSVF 257	
OY	113 LSRSPED-LPIRKSPPTTCLAVDLPASKGYTNLWMSRASCQPVNHSHTSTKEEKKORNGTLT 171	
Db	258 IPRPKRYLVLTITLPRKTCVAVDLSKDDPEQVQSFMDVDVEVHTAQTQVPRREGQNSTSR 317	
OY	172 VTSTLPVGRDWIEGETGYQCRVTHPHLPRALMRSTTKTSGPRAAEVYAFATPEMPSGD 231	
Db	318 SVSELPRIHQWMLNKGKFKCRVNSAAPAPRIEKTISTKSGRKPAPQVYTIIPRKPQMAKD 377	
OY	232 KRTLAQLIONPEPDISVQWLHNEYQLPDAHSTTQPRKTKSGGFVVSRLVYTRAEWQ 291	
Db	378 KVSLLCMITDEPFEEDITVEWMQNN--GQPAENYKNQPTIMDTDGSFYFISKLVOKSMWEA 435	
OY	292 KDEFLICRAVHEAASPQTVRAVSNVPGK 320	
Db	436 GNTFFCSVLHESGLHNHHT-EKSLSSPGK 463	

RESULT 6			
09BOB8	PRELIMINARY:	PRF:	597 AA.
ID 09BOB8			
AC 09BOB8;			
DT 01-JUN-2001 (TRENBLREL. 17, Created)			
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)			
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
NCBI_TaxId=9606;			
NP [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=MUSCLE;			
RA Strausberg R.;			
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RC TISSUE=LYMPH;			
RA Strausberg R.;			
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.			
DR EMBL; BC006180; AAH06180.1; -			
DR EMBL; BC001872; AAH01872.1; -			
DR HSSP; P01825; 7FAB.			
DR InterPro: IPR003599; IG			
DR InterPro: IPR003597; IG_C1			
DR InterPro: IPR003600; IG_1ike			
DR InterPro: IPR003006; IG_MHC			
DR InterPro: IPR003596; IG_V			
DR Pfam: PF00047; Ig; 5			
DR SMART; SM00407; IG; 2			
DR SMART; SM00407; IGC1; 4			
DR SMART; SM00406; IGV; 1			
DR SMART; SM00410; IG_1ike; 1			
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3			
SO SEQUENCE 597 AA; 65300 MW; 2DAFAU50A6375851 CRC64;			
Query Match	24.2%;	Score 413;	DB 4; Length 597;
Best Local Similarity	28.7%;	Pred. No. 3,9e-29;	
Matches 94; Conservative	63;	Mismatches 159;	Indels 12; Gaps 8;

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramodoullah A.K.M., Mista S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)."
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF152372; AAD40243.1; -
DR HSP: P01842; 7FAB.
DR MGD: MGI:96446; Igh-4.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IgV_1.
DR SMART: SM00410; Ig_Like; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 437 1
FT SEQUENCE 437 AA; 48142 MW; 5C3A7B3BE7D697C CRC64;
SO
Query Match 24.1%; Score 411; DB 11; Length 437;
Best Local Similarity 29.5%; Pred. No. 3.9e-29;
Matches 97; Conservative 59; Mismatches 155; Indels 18; Gaps 7;
QY 2 TPPTVTKLQSSCDGGHFPPTIQLCLVSGYTPGTINTWLEDQGVMDVLDSTASTQEG 61
DB 117 TPSPVPLAPG--SAAQTNSKVTGLCVKGFPEPVTVW--NSGSLSSGHTPAVLQS 172
QY 62 ELASTOSELTLQKHWLSDRTYTCQVYTGHTF-----EDSTKCADSNRGVSAY 112
DB 173 DLYTLSSSVTPSTWSE--TVICNVAHNPASTVKDKIYPRDGCPCICTVEVSSVF 231
QY 113 LSRSPSPD-LFIRKSPITTCLVNLDAPSKGVNLWTSRASKPVNHSSTREKORNGTLT 171
DB 232 IFPPKPRDVLITLTLPKVTGVVDISKDDEVPQSFSDVDEVTATQTPREQFNSTFR 291
QY 172 VTSLPVGTMDIEGTYGOCRVTHPHLPRALMRSTTKSGRAPAYAFATPMPGSRD 231
DB 292 SVSELPIMHODWMLNGKEKCRVNSAPAPLEKTIKTKGPRAPQVYITIPPEQMAKD 351
QY 232 KRTIACLIQNMPEPDISVQWLNHEVOLPDARHSTTOPRKTGSGFFVFSRLVTRAEMQ 291
DB 352 KVSITCMTIDFEPPDIYEWQWN--GQPAENYKMTQPIIMDDSGYFYASKNLVQKSNWEA 409
QY 292 KDEFCRAVHEAASPSQTVORAVSVNGK 320
DB 410 GNTFTCSVLHGLHNHHT-EKNLSHSPGK 437
RESULT 10
Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Hypothetical 64.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPH;

RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019235; AAH19235.1; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_5.
DR SMART: SM00409; IgC_2.
DR SMART: SM00407; IgC1_4.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SO SEQUENCE 588 AA; 64438 MW; FC60BDAD82B39FD7 CRC64;
Query Match 23.7%; Score 404; DB 4; Length 588;
Best Local Similarity 28.6%; Pred. No. 2.5e-28;
Matches 92; Conservative 62; Mismatches 156; Indels 12; Gaps 8;
QY 3 PPVTKLQSSCDGGHFPPTIQLCLVSGYTPGTINTWLEDQGVMDVLDSTASTQEG 62
DB 254 PPKVSVFVPPRDGFGNPKRSKLTICQATGFSPTQVSWLREKQVSGVTTDOVQAEAK 313
QY 63 LA-----STQSELTLQKHWLSDRTYTCQVYTGHTF-EDSTKCADSNRGVSAYLSRP 116
DB 314 ESGPTTKVYSTLTIKKSDMLQSMFTCRVDHRLFTQQAASSMCVDDQTAIRVFAIP 373
QY 117 SPFDLFRKSPITTCLVNLDAPSKGVNLWTSRASKPVNHSSTREKORNGTLTIVSTL 176
DB 374 SFASIFLTKSTKLCLVTLDTL-TYDSVTISWTRNGAVVTHNIISSHPATFSAVGEA 432
QY 177 PVGRMDIEGTYGOCRVTHPHLPRALMRSTTKSGPRA-APEVYAF-ATPEMPGSRDRT 234
DB 433 SICEDDMNSGERFTCYTHDLPRLKOTISRPQVALNRPDYLLPAPQQLNRKSAT 492
QY 493 ITCLVTFGSFADVQVQMMORQPLSPKRYVSAPMPQAPAGRFASHILTVSEEWNTG 552
DB 293 DEFCRAVHEAASPSQTVORAV 314
QY 553 EYTCVVAHEAL-PNRVTERIV 573
RESULT 11
Q96EY0 PRELIMINARY; PRT; 613 AA.
AC Q96EY0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Unknown (protein for MGC:20337).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-B-CELL;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011857; AAH11857.1; -
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_5.
DR SMART: SM00408; IgC2_2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SO SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
Query Match 23.7%; Score 404; DB 4; Length 613;
Best Local Similarity 28.6%; Pred. No. 2.7e-28;
Matches 92; Conservative 62; Mismatches 156; Indels 12; Gaps 8;

```
QY 3 PPTVKILQSSCDGGHPPPTIQLCLVSGTPTGNTINTWLEDGQVMDVLDSTASTOEGE 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 PPKVSVFVPPRDGFFGNPRKSKLICOATGSPROIOVSWLNEGKOVSGVTTDQVQAEK 308
QY 63 LA-----STQSELTLSQKHWLSDRTYTCQVYGOCHF-EDSTKCADSNPRGVSAYLSRP 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 309 ESGPTTKYKVTSTLTIKESDMLSQSMFTCRVDHKGTLTQUNASSMCVDPDQTAIRVFAIRP 368
QY 117 SPFDLFRKSPPTTCLVVDLAPSKGVNLWMSRASKGVNHSRKEKORNGTLVTSTL 176
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 SFASIFLTCKSTKLCLVTDLT-TYDSVTLSWTRONGEAVVHTNINISHPNATFSAVGEA 427
QY 177 PVGTRDMEBETVOCRTHTHLPRLMRSTTKTSGPRA-APEYVAF-ATPEMGSRDKRT 234
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 428 SICEDWNSEGRFTCTVTHDLPSPILKOTISRPGVALHRPDVYLLPPAREQLNLRRESAT 487
QY 235 LACLIQFMEDISVQWLHNEVQLPDARHSTTOPR-KTKGSG-FEVFSRLVETRAEWEOK 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 488 ITCLVTFSPADVFVQWOMOGQPLSPKRYTSAPMPERQAPGRYFAHSILTVEEEMWNTG 547
QY 293 DEFICRAVHEAASPSQTVQRAV 314
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Db 548 EYTCVVAHEAL-PNRVTERTV 568
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RESULT 12

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08WUK1 PRELIMINARY; PRT; 613 AA.
ID 08WUK1
AC 08WUK1;
DT 01-MAR-2002 (TReMBrel, 20, Created)
DT 01-MAR-2002 (TReMBrel, 20, Last sequence update)
DT 01-JUN-2002 (TReMBrel, 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1;
DR InterPro: IPR003599; Iq_1;
DR InterPro: IPR003597; Iq_C1;
DR InterPro: IPR003506; Iq_MHC;
DR InterPro: IPR003596; Iq_V;
DR Pfam: PF00047; Iq; 5;
DR SMART; SM00409; Iq; 2;
DR SMART; SM00406; Iq; 1;
DR PROSITE; PS00290; Iq_MHC; UNKNOWN_3;
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
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Query Match 23.7%; Score 404; DB 4; Length 613;

Best Local Similarity 28.6%; Pred. No. 2.7e-28; Matches 92; Conservative 62; Mismatches 156; Indels 12; Gaps 8;

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QY 3 PPTVKILQSSCDGGHPPPTIQLCLVSGTPTGNTINTWLEDGQVMDVLDSTASTOEGE 62
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Db 249 PPKVSVFVPPRDGFFGNPRKSKLICOATGSPROIOVSWLNEGKOVSGVTTDQVQAEK 308
QY 63 LA-----STQSELTLSQKHWLSDRTYTCQVYGOCHF-EDSTKCADSNPRGVSAYLSRP 116
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Db 309 ESGPTTKYKVTSTLTIKESDMLSQSMFTCRVDHKGTLTQUNASSMCVDPDQTAIRVFAIRP 368
QY 117 SPFDLFRKSPPTTCLVVDLAPSKGVNLWMSRASKGVNHSRKEKORNGTLVTSTL 176
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QY 177 PVGTRDMEBETVOCRTHTHLPRLMRSTTKTSGPRA-APEYVAF-ATPEMGSRDKRT 234
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Db 428 SICEDWNSEGRFTCTVTHDLPSPILKOTISRPGVALHRPDVYLLPPAREQLNLRRESAT 487
QY 235 LACLIQFMEDISVQWLHNEVQLPDARHSTTOPR-KTKGSG-FEVFSRLVETRAEWEOK 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 488 ITCLVTFSPADVFVQWOMOGQPLSPKRYTSAPMPERQAPGRYFAHSILTVEEEMWNTG 547
QY 293 DEFICRAVHEAASPSQTVQRAV 314
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Db 548 EYTCVVAHEAL-PNRVTERTV 568
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RESULT 13

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096GA6 PRELIMINARY; PRT; 614 AA.
ID 096GA6
AC 096GA6;
DT 01-DEC-2001 (TReMBrel, 19, Created)
DT 01-DEC-2001 (TReMBrel, 19, Last sequence update)
DT 01-MAR-2002 (TReMBrel, 20, Last annotation update)
DE Unknown (protein for MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1;
DR InterPro: IPR000005; HTHAAC;
DR InterPro: IPR003598; Iq_C2;
DR InterPro: IPR003506; Iq_MHC;
DR Pfam; PF00047; Iq; 5;
DR SMART; SM00408; IqC2; 2;
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1;
DR PROSITE; PS00290; Iq_MHC; UNKNOWN_3;
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
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Query Match 23.7%; Score 404; DB 4; Length 614;

Best Local Similarity 28.6%; Pred. No. 2.7e-28; Matches 92; Conservative 62; Mismatches 156; Indels 12; Gaps 8;

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QY 63 LA-----STQSELTLSQKHWLSDRTYTCQVYGOCHF-EDSTKCADSNPRGVSAYLSRP 116
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Db 310 ESGPTTKYKVTSTLTIKESDMLSQSMFTCRVDHKGTLTQUNASSMCVDPDQTAIRVFAIRP 369
QY 117 SPFDLFRKSPPTTCLVVDLAPSKGVNLWMSRASKGVNHSRKEKORNGTLVTSTL 176
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QY 177 PVGTRDMEBETVOCRTHTHLPRLMRSTTKTSGPRA-APEYVAF-ATPEMGSRDKRT 234
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Db 429 SICEDWNSEGRFTCTVTHDLPSPILKOTISRPGVALHRPDVYLLPPAREQLNLRRESAT 488
QY 235 LACLIQFMEDISVQWLHNEVQLPDARHSTTOPR-KTKGSG-FEVFSRLVETRAEWEOK 292
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QY 293 DEFICRAVHEAASPSQTVQRAV 314
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Db 549 EYTCVVAHEAL-PNRVTERTV 569
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RESULT 14

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ID 096AA6
AC 096AA6;
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DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical 67.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAI17356.1; -
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00408; IgC2; 1.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 618 AA; 67758 MW; 96DBDAC7C696E0A6 CRC64;

Query Match 23.7%; Score 404; DB 4; Length 618;
Best Local Similarity 28.6%; Pred. No. 2.7e-28;
Matches 92; Conservative 62; Mismatches 156; Indels 12; Gaps 8;

QY 3 PPVTIKILOSQCDGGHPPTIOLCLVSGYPTGNTINIMLEDGOVMDVLDSTASTQGE 62
DB 254 PPKSVTFPPRDGFFGNPKRKLICQATGSPROIQVSMLEKQVSGVTTDOYQAFK 313
QY 63 LA-----STOSELTLISQKHWLSDRTYTCQVYQGHTE-EDSTKCADSNPRGVSAYLSRP 116
DB 314 ESGPTTKVSTLTILKESDWLSQSMFTCRVDHRTLFQNASMKVPPQDTAIRFAIRP 373
QY 117 SPFLFIKRSPTTICLVVDLAPSKGYVLTMSRASKGVNHSSTKREKQNGTILVSTL 176
DB 374 SPASIFLTKSKTLCVLVDLQ-TYDSVTISWTRONGEAVKTHNISESHPNATPSAVGEA 432
QY 177 PVGTRDWIEGETYOCRVTHPHLPALMRSTTKTSQPR-APEVYAF-ATPMPGSRDKRT 234
DB 433 SICDDNMNSGERFCTVHTDLPRLKOTISRPGVALHRDVIILPPARQOLNRESAT 492
QY 235 LACLIQNFMPEDISVQWILHNEVOLPDARHSTQPR-KTKGSG-PFVFSRLVTRAWEOK 292
DB 493 ITCLVTFGSPADVQWQRCQPLSPKXYTSAPEPQAPGRYFAHSILTVSEEWNTG 552
QY 293 DEFICRAVHEASPSQYQRAV 314
DB 553 ETVTCVAHREAL-PKRTERTV 573

RESULT 15
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ID 099L31 PRELIMINARY; PRT; 468 AA.
AC 099L31;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA03878.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig_
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 23.6%; Score 402; DB 11; Length 468;
Best Local Similarity 28.6%; Pred. No. 2.8e-28;
Matches 97; Conservative 63; Mismatches 147; Indels 32; Gaps 8;

QY 2 PPVTIKILOSQCDGGHPPTIOLCLVSGYPTGNTINIMLEDGOVMDVLDSTASTQEG 61
DB 142 TAPSVYPLAPVC--GDTTGSVTLGCLVKGTFPEPVILTW--NNGSLSSGHTTPAVLQS 197
QY 62 ELASTQSELTLISQKHWLSDRTYTCQVYQGHTEFEDSTKCADSNPRGVA----- 111
DB 198 DLYTLSSSVTVSTSTWPS-QSITCNVAHPA-----SFTKVDKRIEPRGPTIKPCPPCKPA 252
QY 112 --YLSRSPF-----DLFIKSPITTCLVVDLAPSKGYVLTMSRASKGVNHSSTRK 161
DB 253 PNLGGPSVFTFPKIKVDVLMISLSPMTCVVVDVSEDDPDVQISWFVNNVETLAQTOT 312
QY 162 EEKQNGTILVTVSTLPVGTQDMIEGETYOCRVTHPHLPALMRSTTKTSQPRAPEVYAF 221
DB 313 HREDYNSTLRVYSALPIOHODMMSKKEFKCVNNKALPAPLERTISKSGSVRAQYVL 372
QY 222 ATPMPGSRDKRTLACLIQNFMPEDISVQWILHNEVOLPDARHSTQPRKTKGSGFEVFSR 281
DB 373 PPPEEEMTKKQVTLTCWTDPMPEDIYEWETNN--GKTELNYKNTPEVLDSGGSYFMSK 430
QY 282 LEVTRAWEOKDEFICRAVHEASPSQYQRAVSVNPECK 320
DB 431 LVEKKNVKNRSTSCSVYHEGLHNHHTT-KFSKTPCK 468

Search completed: July 15, 2003, 07:01:48
Job time : 36.9679 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: July 15, 2003, 06:59:40 ; Search time 24.5495 Seconds
(without alignments)
1517.518 Million cell updates/sec

Title: US-09-847-208B-6
Perfect score: 1707
Sequence: 1 FTPTVKILQSSCDGCGHFP.....HEAASPSQTVQRAVSVPNGK 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	320	US-09-847-208-6	Sequence 6, Appli
2	1707	100.0	323	US-09-949-375A-2	Sequence 2, Appli
3	1707	100.0	323	US-09-949-375A-4	Sequence 4, Appli
4	1707	100.0	323	US-09-949-375A-6	Sequence 6, Appli
5	1707	100.0	331	US-10-176-664-1	Sequence 1, Appli
6	1707	100.0	331	US-10-207-655-329	Sequence 329, App
7	1707	100.0	331	US-09-401-636-1	Sequence 1, Appli
8	1707	100.0	427	US-09-847-208-5	Sequence 5, Appli
9	1707	100.0	428	US-10-047-542-60	Sequence 60, Appl
10	1707	100.0	428	US-09-949-375A-1	Sequence 1, Appli
11	1707	100.0	428	US-09-916-230-1	Sequence 1, Appli
12	1707	100.0	569	US-09-847-208-7	Sequence 7, Appli
13	1707	100.0	574	US-10-047-542-45	Sequence 45, Appl
14	1707	100.0	574	US-10-214-524-37	Sequence 37, Appl
15	1707	100.0	592	US-10-207-655-334	Sequence 334, App
16	1696	99.4	336	US-09-949-375A-8	Sequence 8, Appli
17	1696	99.4	441	US-09-949-375A-7	Sequence 7, Appli
18	1671	97.9	330	US-09-949-375A-10	Sequence 10, Appl
19	1649	96.6	347	US-10-152-190-13	Sequence 13, Appl

20	1644.5	96.3	426	US-10-214-524-26	Sequence 26, Appl
21	1579	92.5	347	US-10-152-190-12	Sequence 12, Appl
22	1566.5	91.8	348	US-10-152-190-11	Sequence 11, Appl
23	1435.5	84.1	346	US-10-152-190-10	Sequence 10, Appl
24	1364.5	79.9	346	US-10-152-190-14	Sequence 14, Appl
25	1158	67.8	222	US-09-809-715-6	Sequence 6, Appli
26	1158	67.8	222	US-09-809-746-2	Sequence 2, Appli
27	1038.5	60.8	342	US-10-176-664-8	Sequence 8, Appli
28	1038.5	60.8	342	US-09-401-636-8	Sequence 8, Appli
29	1011.5	59.3	236	US-10-152-190-9	Sequence 9, Appli
30	956.5	56.0	426	US-10-214-524-28	Sequence 28, Appl
31	955.5	56.0	496	US-10-214-524-25	Sequence 25, Appl
32	949.5	55.6	431	US-09-479-614-14	Sequence 14, Appl
33	949.5	55.6	496	US-09-479-614-2	Sequence 2, Appli
34	949.5	55.6	496	US-09-479-614-29	Sequence 29, Appl
35	906.5	53.1	569	US-10-214-524-30	Sequence 30, Appl
36	827	48.4	341	US-10-176-664-11	Sequence 11, Appl
37	827	48.4	341	US-09-401-636-11	Sequence 11, Appl
38	823	48.2	563	US-10-214-524-35	Sequence 35, Appl
39	804	47.1	567	US-10-214-524-33	Sequence 33, Appl
40	793	46.5	340	US-10-176-664-2	Sequence 2, Appli
41	793	46.5	340	US-09-401-636-2	Sequence 2, Appli
42	793	46.5	428	US-10-214-524-34	Sequence 34, Appl
43	788.5	46.2	426	US-10-214-524-27	Sequence 27, Appl
44	781	45.8	341	US-10-176-664-3	Sequence 3, Appli
45	781	45.8	341	US-09-401-636-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1				
US-09-847-208-6				
Sequence 6, Application US/09847208				
Publication NO. US20030082190A1				
GENERAL INFORMATION:				
APPLICANT: Saxon, Andrew				
APPLICANT: Zhu, Daocheng				
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF				
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES				
FILE REFERENCE: UC67.002A				
CURRENT APPLICATION NUMBER: US/09/847,208				
CURRENT FILING DATE: 2001-05-01				
NUMBER OF SEQ ID NOS: 177				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 6				
LENGTH: 320				
TYPE: PRT				
ORGANISM: Homo sapiens				
US-09-847-208-6				
Query Match				
Best Local Similarity 100.0%; Pred. No. 8.3e-122;				
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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QY	121	LFIRKSPITTCVYDLAPSKGVNLTWSASGKPVNHSTRKEKORNGTLVTSPLPGT	180	
DB	121	LFIRKSPITTCVYDLAPSKGVNLTWSASGKPVNHSTRKEKORNGTLVTSPLPGT	180	
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QY      301 HEASPSQTVORAVSNPGK 320
Db      301 HEASPSQTVORAVSNPGK 320

RESULT 2
US-09-949-375A-2
; Sequence 2, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949, 375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (8)..(103)
; OTHER INFORMATION: Human IGE heavy chain C2 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)..(211)
; OTHER INFORMATION: Human IGE heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (216)..(317)
; OTHER INFORMATION: Human IGE heavy chain C4 domain
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; NAME/KEY: MISC_FEATURE
; LOCATION: (104)..(111)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (212)..(215)
; OTHER INFORMATION: Linker between domains C3 and C4
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; NAME/KEY: MISC_FEATURE
; LOCATION: (100)..(114)
; OTHER INFORMATION: Epitope including C2C3 linker
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; NAME/KEY: MISC_FEATURE
; LOCATION: (210)..(218)
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; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (139)..(145)
; OTHER INFORMATION: Epitope in BC loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (167)..(175)
; OTHER INFORMATION: Epitope in DE loop
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; NAME/KEY: MISC_FEATURE
; LOCATION: (196)..(206)
; OTHER INFORMATION: Epitope in FG loop
; US-09-949-375A-2

Query Match      100.0%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      61 GELASTOSELTLSQKHWLSDRTYTTCQVTTYOGHTFEDSTKKCADSNPBGVSAYLSRPSPF 120
Db      64 GELASTOSELTLSQKHWLSDRTYTTCQVTTYOGHTFEDSTKKCADSNPBGVSAYLSRPSPF 123
QY      121 LFIKSPITICLVVDLAPSKGTVNLWTSRSGKRVNHNSTRKEEKORNGTLLVTSITLVGT 180
Db      124 LFIKSPITICLVVDLAPSKGTVNLWTSRSGKRVNHNSTRKEEKORNGTLLVTSITLVGT 183
QY      181 RDWIEGETYOCRVYTHPLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db      184 RDWIEGETYOCRVYTHPLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTLACLIQ 243
QY      241 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGFFVFSRLLEVTRAEMEDKDEFICRAV 300
Db      244 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGFFVFSRLLEVTRAEMEDKDEFICRAV 303
QY      301 HEASPSQTVORAVSNPGK 320
Db      304 HEASPSQTVORAVSNPGK 323

RESULT 3
US-09-949-375A-4
; Sequence 4, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949, 375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3.
; US-09-949-375A-4

Query Match      100.0%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

; Sequence 6, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949, 375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5.
US-09-949-375A-6

Query Match 100.0%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8,4e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTPGTINITWLEQGVNDVLDSTASTQ 60
DB 4 FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTPGTINITWLEQGVNDVLDSTASTQ 63
QY 61 GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRPSFD 120
DB 64 GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRPSFD 123
QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEORNGTLTVSTLPVGT 180
DB 124 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEORNGTLTVSTLPVGT 183
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSRDKRTLACLIQ 240
DB 184 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSRDKRTLACLIQ 243
QY 241 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLEVTRAEMQKDEFICRAV 300
DB 244 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLEVTRAEMQKDEFICRAV 303
QY 301 HEAASPSQTVQRAVSVNPGK 320
DB 304 HEAASPSQTVQRAVSVNPGK 323

RESULT 5
US-10-176-664-1

; Sequence 1, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176, 664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401, 636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106, 652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-1

Query Match 100.0%; Score 1707; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8,6e-122;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTPGTINITWLEQGVNDVLDSTASTQ 60
DB 12 FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTPGTINITWLEQGVNDVLDSTASTQ 71
QY 61 GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRPSFD 120
DB 72 GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRPSFD 131
QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEORNGTLTVSTLPVGT 180
DB 132 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEORNGTLTVSTLPVGT 191
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSRDKRTLACLIQ 240
DB 192 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSRDKRTLACLIQ 251
QY 241 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLEVTRAEMQKDEFICRAV 300
DB 252 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLEVTRAEMQKDEFICRAV 311
QY 301 HEAASPSQTVQRAVSVNPGK 320
DB 312 HEAASPSQTVQRAVSVNPGK 331

RESULT 6
US-10-207-655-329

; Sequence 329, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069, 401C1
; CURRENT APPLICATION NUMBER: US/10/207, 655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 329
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-329

Query Match 100.0%; Score 1707; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8,6e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTPGTINITWLEQGVNDVLDSTASTQ 60
DB 8 FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTPGTINITWLEQGVNDVLDSTASTQ 67
QY 61 GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRPSFD 120
DB 68 GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRPSFD 127
QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEORNGTLTVSTLPVGT 180
DB 128 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEORNGTLTVSTLPVGT 187
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSRDKRTLACLIQ 240
DB 188 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSRDKRTLACLIQ 247
QY 241 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLEVTRAEMQKDEFICRAV 300
DB 248 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLEVTRAEMQKDEFICRAV 307
QY 301 HEAASPSQTVQRAVSVNPGK 320

|||||
Db 308 HEAASPSQTVQRAVSVPNGK 327

RESULT 7

US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-1

Query Match 100.0%; Score 1707; DB 10; Length 331;
Best Local Similarity 100.0%; Pred. No. 8.6e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILOSCDGGHFPPTIQLCLVSGYTPGTINITWLEBDGQVMDVLDSTASTTQE 60
Db 12 FTPTVKIILOSCDGGHFPPTIQLCLVSGYTPGTINITWLEBDGQVMDVLDSTASTTQE 71
QY 61 GELASTOSELTLISQKHWLSDRTYTCQVYOGHTEFEDSTKRCADSNPRGVSAYLSRSPFD 120
Db 72 GELASTOSELTLISQKHWLSDRTYTCQVYOGHTEFEDSTKRCADSNPRGVSAYLSRSPFD 131
QY 121 LFTKRSPTITCLVVDLAPSKGYNLWTSRASGKPVNHSRSTKEKORNGTLTVSTLPVGT 180
Db 132 LFTKRSPTITCLVVDLAPSKGYNLWTSRASGKPVNHSRSTKEKORNGTLTVSTLPVGT 191
QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKTSGPRAAPEVYAFAPPEWGSDDKRTLACLIQ 240
Db 192 RDWIEGETYOCRVTHPHLPALMRSTTKTSGPRAAPEVYAFAPPEWGSDDKRTLACLIQ 251
QY 241 NFMPEDISVQMLHNEVQLPDARHSTTQPRKTKSGFVFESRLLEYTRAEMQKDEFICRAV 300
Db 252 NFMPEDISVQMLHNEVQLPDARHSTTQPRKTKSGFVFESRLLEYTRAEMQKDEFICRAV 311
QY 301 HEAASPSQTVQRAVSVPNGK 320
Db 312 HEAASPSQTVQRAVSVPNGK 331

RESULT 8

US-09-847-208-5
; Sequence 5, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daosheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 427
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-847-208-5

Query Match 100.0%; Score 1707; DB 9; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.2e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILOSCDGGHFPPTIQLCLVSGYTPGTINITWLEBDGQVMDVLDSTASTTQE 60
Db 108 FTPTVKIILOSCDGGHFPPTIQLCLVSGYTPGTINITWLEBDGQVMDVLDSTASTTQE 167
QY 61 GELASTOSELTLISQKHWLSDRTYTCQVYOGHTEFEDSTKRCADSNPRGVSAYLSRSPFD 120
Db 168 GELASTOSELTLISQKHWLSDRTYTCQVYOGHTEFEDSTKRCADSNPRGVSAYLSRSPFD 227
QY 121 LFTKRSPTITCLVVDLAPSKGYNLWTSRASGKPVNHSRSTKEKORNGTLTVSTLPVGT 180
Db 228 LFTKRSPTITCLVVDLAPSKGYNLWTSRASGKPVNHSRSTKEKORNGTLTVSTLPVGT 287
QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKTSGPRAAPEVYAFAPPEWGSDDKRTLACLIQ 240
Db 288 RDWIEGETYOCRVTHPHLPALMRSTTKTSGPRAAPEVYAFAPPEWGSDDKRTLACLIQ 347
QY 241 NFMPEDISVQMLHNEVQLPDARHSTTQPRKTKSGFVFESRLLEYTRAEMQKDEFICRAV 300
Db 348 NFMPEDISVQMLHNEVQLPDARHSTTQPRKTKSGFVFESRLLEYTRAEMQKDEFICRAV 407
QY 301 HEAASPSQTVQRAVSVPNGK 320
Db 408 HEAASPSQTVQRAVSVPNGK 427

RESULT 9

US-10-047-542-60
; Sequence 60, Application US/10047542
; Patent No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; FILE REFERENCE: 030905.0004.C1P1
; CURRENT APPLICATION NUMBER: US/10/047.542
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200.298
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-60

Query Match 100.0%; Score 1707; DB 9; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.2e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILOSCDGGHFPPTIQLCLVSGYTPGTINITWLEBDGQVMDVLDSTASTTQE 60
Db 109 FTPTVKIILOSCDGGHFPPTIQLCLVSGYTPGTINITWLEBDGQVMDVLDSTASTTQE 168
QY 61 GELASTOSELTLISQKHWLSDRTYTCQVYOGHTEFEDSTKRCADSNPRGVSAYLSRSPFD 120
Db 169 GELASTOSELTLISQKHWLSDRTYTCQVYOGHTEFEDSTKRCADSNPRGVSAYLSRSPFD 228
QY 121 LFTKRSPTITCLVVDLAPSKGYNLWTSRASGKPVNHSRSTKEKORNGTLTVSTLPVGT 180
Db 229 LFTKRSPTITCLVVDLAPSKGYNLWTSRASGKPVNHSRSTKEKORNGTLTVSTLPVGT 288
QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKTSGPRAAPEVYAFAPPEWGSDDKRTLACLIQ 240

Db 289 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 348
QY 241 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEYTRAWEOKDEFICRAV 300
Db 349 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEYTRAWEOKDEFICRAV 408
QY 301 HEAASPSQTVORAVSVNPGK 320
Db 409 HEAASPSQTVORAVSVNPGK 428

RESULT 10
US-09-949-375A-1
Sequence 1, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 428
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (11)..(116)
OTHER INFORMATION: Human Ige heavy chain C1 domain
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (209)..(216)
OTHER INFORMATION: Linker between domains C2 and C3
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (205)..(219)
OTHER INFORMATION: Epitope including C2C3 linker
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (244)..(251)
OTHER INFORMATION: Epitope in BC loop
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (272)..(280)
OTHER INFORMATION: Epitope in DE loop
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (301)..(311)
OTHER INFORMATION: Epitope in FG loop
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (317)..(320)
OTHER INFORMATION: Linker between domains C3 and C4
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (321)..(422)
OTHER INFORMATION: Human Ige heavy chain C4 domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (217)..(316)
OTHER INFORMATION: Human Ige heavy chain C3 domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (113)..(208)
OTHER INFORMATION: Human Ige heavy chain C2 domain
US-09-949-375A-1

Query Match 100.0%; Score 1707; DB 9; Length 428;
Best Local Similarity 100.0%; Pred. No. 1,2e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPTPVKILQSSCDGGGHFPPTIQLCLVSGTPTGINTITWLEDGQVMDVDLSTASTQOE 60
Db 109 FTPTPVKILQSSCDGGGHFPPTIQLCLVSGTPTGINTITWLEDGQVMDVDLSTASTQOE 168
QY 61 GELASTQSELTLSOKHMLSDRTYTCQVYQGHTEFEDSTKCADSNPRGVSAYLSRPSFD 120
Db 169 GELASTQSELTLSOKHMLSDRTYTCQVYQGHTEFEDSTKCADSNPRGVSAYLSRPSFD 228
QY 121 LFIKRSPTITCLVVDLAPSKGTVALTWASRAGKPVNHSRKEERKORNGTLVTSTLPVGT 180
Db 229 LFIKRSPTITCLVVDLAPSKGTVALTWASRAGKPVNHSRKEERKORNGTLVTSTLPVGT 288
QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 240
Db 289 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 348
QY 241 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEYTRAWEOKDEFICRAV 300
Db 349 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEYTRAWEOKDEFICRAV 408
QY 301 HEAASPSQTVORAVSVNPGK 320
Db 409 HEAASPSQTVORAVSVNPGK 428

RESULT 11
US-09-916-230-1
Sequence 1, Application US/09916230
Patent No. US20020146422A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
TITLE OF INVENTION: Compositions for Inducing Self-Specific Anti-Ige
FILE REFERENCE: 1700.0140001
CURRENT APPLICATION NUMBER: US/09/916,230
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/221,841
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-916-230-1

Query Match 100.0%; Score 1707; DB 10; Length 428;
Best Local Similarity 100.0%; Pred. No. 1,2e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPTPVKILQSSCDGGGHFPPTIQLCLVSGTPTGINTITWLEDGQVMDVDLSTASTQOE 60
Db 109 FTPTPVKILQSSCDGGGHFPPTIQLCLVSGTPTGINTITWLEDGQVMDVDLSTASTQOE 168
QY 61 GELASTQSELTLSOKHMLSDRTYTCQVYQGHTEFEDSTKCADSNPRGVSAYLSRPSFD 120
Db 169 GELASTQSELTLSOKHMLSDRTYTCQVYQGHTEFEDSTKCADSNPRGVSAYLSRPSFD 228
QY 121 LFIKRSPTITCLVVDLAPSKGTVALTWASRAGKPVNHSRKEERKORNGTLVTSTLPVGT 180
Db 229 LFIKRSPTITCLVVDLAPSKGTVALTWASRAGKPVNHSRKEERKORNGTLVTSTLPVGT 288
QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 240
Db 289 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 348
QY 241 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEYTRAWEOKDEFICRAV 300

|||||
Db 349 NFMEDISVOMLHNEVQLPDARHSTTOPRRTKSGGFVFSRLLEVTRAEMQKDEFICRAV 408
QY 301 HEAASPSQTVORAVSNPGR 320
|||||
Db 409 HEAASPSQTVORAVSNPGR 428

RESULT 12

US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67 002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; NUMBER OF FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
; OTHER INFORMATION: (Ige)
US-09-847-208-7

Query Match 100.0%; Score 1707; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.6e-121;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQOE 60
|||||
Db 250 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQOE 309
61 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 120
|||||
Db 310 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 369
121 LFIKRSPTITCLVVDLAPSKGYVNLWTSRASKPVNHSKKEKORNGTLTVSTLPVGT 180
|||||
Db 370 LFIKRSPTITCLVVDLAPSKGYVNLWTSRASKPVNHSKKEKORNGTLTVSTLPVGT 429
181 RDMIEGTYOCRTYHPLPRALMRSTKTSGRAPAEVYAFATPEWPGSDKRTLACTLIQ 240
|||||
Db 430 RDMIEGTYOCRTYHPLPRALMRSTKTSGRAPAEVYAFATPEWPGSDKRTLACTLIQ 489
QY 241 NFMEDISVOMLHNEVQLPDARHSTTOPRRTKSGGFVFSRLLEVTRAEMQKDEFICRAV 300
|||||
Db 490 NFMEDISVOMLHNEVQLPDARHSTTOPRRTKSGGFVFSRLLEVTRAEMQKDEFICRAV 549
QY 301 HEAASPSQTVORAVSNPGR 320
|||||
Db 550 HEAASPSQTVORAVSNPGR 569

RESULT 13

US-10-047-542-45
; Sequence 45, Application US/10047542
; Patent No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WILCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26

; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-45

Query Match 100.0%; Score 1707; DB 9; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.6e-121;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQOE 60
|||||
Db 255 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQOE 314
61 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 120
|||||
Db 315 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 374
121 LFIKRSPTITCLVVDLAPSKGYVNLWTSRASKPVNHSKKEKORNGTLTVSTLPVGT 180
|||||
Db 375 LFIKRSPTITCLVVDLAPSKGYVNLWTSRASKPVNHSKKEKORNGTLTVSTLPVGT 434
181 RDMIEGTYOCRTYHPLPRALMRSTKTSGRAPAEVYAFATPEWPGSDKRTLACTLIQ 240
|||||
Db 435 RDMIEGTYOCRTYHPLPRALMRSTKTSGRAPAEVYAFATPEWPGSDKRTLACTLIQ 494
241 NFMEDISVOMLHNEVQLPDARHSTTOPRRTKSGGFVFSRLLEVTRAEMQKDEFICRAV 300
|||||
Db 495 NFMEDISVOMLHNEVQLPDARHSTTOPRRTKSGGFVFSRLLEVTRAEMQKDEFICRAV 554
QY 301 HEAASPSQTVORAVSNPGR 320
|||||
Db 555 HEAASPSQTVORAVSNPGR 574

RESULT 14

US-10-214-524-37
; Sequence 37, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barakiewicz, Theresa J.
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 37
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-37

Query Match 100.0%; Score 1707; DB 9; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.6e-121;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQOE 60
|||||
Db 255 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQOE 314
61 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 120

```
Db      315  GELASTQSELTLSQKHWLSDRTYCCQVYOGHTFEDSTKKCADSNPRGVSAYLSRPSFPD 374
QY      121  LFIKRSPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSTRKKEKQKNGTILVTSTLPVGT 180
Db      375  LFIKRSPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSTRKKEKQKNGTILVTSTLPVGT 434
QY      181  RDWIEGTYOCRTVHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db      435  RDWIEGTYOCRTVHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 494
QY      241  NFMEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLLEVTRAWEQKDEFICRAV 300
Db      495  NFMEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLLEVTRAWEQKDEFICRAV 554
QY      301  HEAASPSQTVQRAVSVNPGK 320
Db      555  HEAASPSQTVQRAVSVNPGK 574
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RESULT 15

```
US-10-207-655-334
; Sequence 334, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 334
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-334
```

Query Match 100.0%; Score 1707; DB 9; Length 592;

Best Local Similarity 100.0%; Pred. No. 1.7e-121;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1  FTPTVVILOSSCGCGGHFPPTIQLCLVSGYTGTTNITWLEDQVMDVDLSTASTTQE 60
Db      273  FTPTVVILOSSCGCGGHFPPTIQLCLVSGYTGTTNITWLEDQVMDVDLSTASTTQE 332
QY      61  GELASTQSELTLSQKHWLSDRTYCCQVYOGHTFEDSTKKCADSNPRGVSAYLSRPSFPD 120
Db      333  GELASTQSELTLSQKHWLSDRTYCCQVYOGHTFEDSTKKCADSNPRGVSAYLSRPSFPD 392
QY      121  LFIKRSPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSTRKKEKQKNGTILVTSTLPVGT 180
Db      393  LFIKRSPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSTRKKEKQKNGTILVTSTLPVGT 452
QY      181  RDWIEGTYOCRTVHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db      453  RDWIEGTYOCRTVHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 512
QY      241  NFMEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLLEVTRAWEQKDEFICRAV 300
Db      513  NFMEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLLEVTRAWEQKDEFICRAV 572
QY      301  HEAASPSQTVQRAVSVNPGK 320
Db      573  HEAASPSQTVQRAVSVNPGK 592
```

Search completed: July 15, 2003, 07:17:19
Job time : 25.5495 secs


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Db      164 EGNVTSHELNITOGWVNSQKTYTCOYTGFTFKDARKCSDDPGVTSYLSPPSL 223
        120 DLFRKSPITITCLVVDLAPSKGTYNLWASRSGKPVNHSRKEKORNGTITVSTLPVG 179
        224 DLYHKAAPKITCLVVDLAPSKGTYNLWASRSGKPVNHSRKEKORNGTITVSTLPVG 282
Qy      180 TRDMEGTTCOYCRVTHPHLPALMRSTTKISGPRAPEVYAFAP-EMPGSRDKRTIACL 238
        283 TNDMEGTTCOYCRVTHPHLPALMRSTTKISGPRAPEVYAFAP-EMPGSRDKRTIACL 342
Db      239 IONFMPEDISVQWLHNEVQLDARHSTTQPRKTKGS--GFVFSRLVETRAEMWOKDEFI 296
        343 IONFMPEDISVQWLHNEVQLDARHSTTQPRKTKGS--GFVFSRLVETRAEMWOKDEFI 402
Qy      297 CRAVHEAASPSQTVORAVSNVPGK 320
        403 CQVYHEALSGSRILQKWKSKTPGK 426
Db
```

RESULT 2

```
PCT-US95-13795-2
: Sequence 2, Application PC/TUS9513795
: GENERAL INFORMATION:
: APPLICANT: HOLLIS, GREGORY F.
: APPLICANT: PATEL, MAYOR D.
: TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CHRISTINE E. CARTY
: STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
: CITY: RAHWAY
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07065-0907
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/13795
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: CARTY, CHRISTINE E.
: REGISTRATION NUMBER: 36,099
: REFERENCE/DOCKET NUMBER: 19211Y
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 594-6734
: TELEFAX: (908) 594-4720
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 426 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-13795-2
```

```
Query Match      56.0%: Score 956.5; DB 5; Length 426;
Best Local Similarity 56.2%: Pred. No. 4.5e-84;
Matches 182; Conservative 50; Mismatches 87; Indels 5; Gaps 4;

Qy      1 FTPTVAKILSSCDGGGHFPTTIOILCLVSGYTPGTINITWL-EDQVMDVLDSTASTQ 59
        104 FIPTVAKILSSCDGGGHFPTTIOILCLVSGYTPGTINITWL-EDQVMDVLDSTASTQ 163
Db      60 EGEIATQSELTLTQKHLMDRTYTCOYTGHTFEDSTKCADSNPRGVSAYLSRPSPF 119
        164 EGNVTSHELNITOGWVNSQKTYTCOYTGFTFKDARKCSDDPGVTSYLSPPSL 223
Qy      120 DLFRKSPITITCLVVDLAPSKGTYNLWASRSGKPVNHSRKEKORNGTITVSTLPVG 179
```

```
Db      224 DLYHKAAPKITCLVVDLAPSKGTYNLWASRSGKPVNHSRKEKORNGTITVSTLPVG 282
        180 TRDMEGTTCOYCRVTHPHLPALMRSTTKISGPRAPEVYAFAP-EMPGSRDKRTIACL 238
        283 TNDMEGTTCOYCRVTHPHLPALMRSTTKISGPRAPEVYAFAP-EMPGSRDKRTIACL 342
Qy      239 IONFMPEDISVQWLHNEVQLDARHSTTQPRKTKGS--GFVFSRLVETRAEMWOKDEFI 296
        343 IONFMPEDISVQWLHNEVQLDARHSTTQPRKTKGS--GFVFSRLVETRAEMWOKDEFI 402
Db      297 CRAVHEAASPSQTVORAVSNVPGK 320
        403 CQVYHEALSGSRILQKWKSKTPGK 426
Db
```

RESULT 3

```
US-09-192-545-2
: Sequence 2, Application US/09192545
: Patent No. 6118044
: GENERAL INFORMATION:
: APPLICANT: Karasuyama, Hajime
: APPLICANT: Yonekawa, Hiromichi
: APPLICANT: Taya, Choji
: APPLICANT: Matsuoaka, Kunie
: TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
: FILE REFERENCE: 799P79570
: CURRENT APPLICATION NUMBER: US/09/192,545
: CURRENT FILING DATE: 1998-11-13
: EARLIER APPLICATION NUMBER: JP HEI 9-313989
: EARLIER FILING DATE: 1997-11-14
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 561
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE: Description of Artificial Sequence: Designed heavy
: US-09-192-545-2
```

```
Query Match      39.7%: Score 678.5; DB 3; Length 561;
Best Local Similarity 43.7%: Pred. No. 4.4e-57;
Matches 136; Conservative 56; Mismatches 112; Indels 7; Gaps 6;
```

```
Qy      13 CDGGHFPPTIOLCLVSGYTPGTINITWL-EDQVMDVLDSTASTQEGELASTQSELT 71
        247 CDPNA-FHSTIQLCYFIYGHILNDVSVSMILDDREITDTLAQTVLIREEGKLASTCSKLN 305
Qy      72 LSKHNLSDRTYTCOYTGHTFEDSTKCADSNPRGVSAYLSRPSPFIRKSPITTC 131
        306 ITTEOWMSESTFTCRVTSQGVYLAHTRRCDFHPRGATITLIPSPDLIXONGAPKLTTC 365
Db      132 LVVDLAPSKGTYNLWASRSGKPVNHSRKEKORNGTITVSTLPVGTDRMIGETVQC 191
        366 LVVDLESK-NVNTYTWQDEKTSVSASQWYTKHNNATSTISITLPPYAKMIGYXQC 424
Qy      192 RYTHPHLPALMRSTTKIS--GPRAPEVYAFATPEWDSRDKRTIACLIONFMPEDISVQ 250
        425 VVDRPDPFKPIVRSITLIPVQSARSAPEYVYVPPPE-ESEEDKRTIACLIONFMPEDISVQ 483
Db      251 WLHNEVQLDARHSTTQPRKTKGS--GFVFSRLVETRAEMWOKDEFCRAVHEAASPSQ 308
        484 WLGGKSLTNSQHSHTTPPLASNGSNQGFIFSRLEVAKTMTQKQKFCOVYHEALQKPR 543
Qy      309 TVORAVSNVPG 319
        544 KLEKTIISTSLG 554
Db
```

```
RESULT 4
US-08-232-539D-56
: Sequence 56, Application US/08232539D
: Patent No. 5965709
```

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardiou, Paula M.
TITLE OF INVENTION: IGE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Syvoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-56

Query Match 35.0%; Score 597; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3e-50;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 CADSNPRGVSAYLSRPSFDFIRKSPITITLVVDLAPSKGTVNLWMSRASKGPNVHSTR 160
|||||
DB 1 CADSNPRGVSAYLSRPSFDFIRKSPITITLVVDLAPSKGTVNLWMSRASKGPNVHSTR 60

QY 161 KEKQRNGTLVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMSTTKTSGP 212
|||||
DB 61 KEKQRNGTLVTSTLPGVTRDWIEGETYQCRVTHPHLPRALMSTTKTSGP 112

RESULT 5
US-08-399-106A-6
Sequence 6, Application US/08399106A
Patent No. 5731168
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,106A
FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0927
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-399-106A-6

Query Match 34.4%; Score 587; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.7e-49;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GPRAAPEYAFATPEWGRSRRKRLACLIOFMEDISVQMLHNEVQLPDRHSTTPRK 270
|||||
DB 1 GPRAAPEYAFATPEWGRSRRKRLACLIOFMEDISVQMLHNEVQLPDRHSTTPRK 60

QY 271 TKGSGFEVSRLEVTTRAEMEQKDEFICRAVHEAASPSQTVQRAVSVPNGK 320
|||||
DB 61 TKGSGFEVSRLEVTTRAEMEQKDEFICRAVHEAASPSQTVQRAVSVPNGK 110

RESULT 6
US-08-433-105A-6
Sequence 6, Application US/08433105A
Patent No. 5807706
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,105A
FILING DATE: 03-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/399106
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0927D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-433-105A-6

Query Match 34.4%; Score 587; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.7e-49;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GPPAAPVYAFATPEWGSRDRTLACLIQNFMPEDISVOMLHNEVOLPDARHSTQPRK 270
DB 1 GPPAAPVYAFATPEWGSRDRTLACLIQNFMPEDISVOMLHNEVOLPDARHSTQPRK 60

QY 271 TKSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 320
DB 61 TKSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 110

RESULT 7

US-08-434-869A-6
Sequence 6, Application US/08434869A
Patent No. 5821333

GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
APPLICANT: Riddway, John B.
TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Mupatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,869A
FILING DATE: 03-May-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/399106
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0927D1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-434-869A-6

Query Match 34.4%; Score 587; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.7e-49;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GPPAAPVYAFATPEWGSRDRTLACLIQNFMPEDISVOMLHNEVOLPDARHSTQPRK 270
DB 1 GPPAAPVYAFATPEWGSRDRTLACLIQNFMPEDISVOMLHNEVOLPDARHSTQPRK 60

QY 271 TKSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 320

DB 61 TKSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 110

RESULT 8

US-08-037-579A-2
Sequence 2, Application US/08037579A
Patent No. 5552537

GENERAL INFORMATION:
APPLICANT: Zhang, Ke
APPLICANT: Max, Edward E
APPLICANT: Saxon, Andrew
TITLE OF INVENTION: IGE ISOFORMS AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,579A
FILING DATE: 24-MAR-1993
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Berttram I
REGISTRATION NUMBER: 20,015

REFERENCE/DOCKET NUMBER: A-57950/BIR UCLA-233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249

TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-037-579A-2

Query Match 34.0%; Score 581; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 PRAAPVYAFATPEWGSRDRTLACLIQNFMPEDISVOMLHNEVOLPDARHSTQPRK 271
DB 1 PRAAPVYAFATPEWGSRDRTLACLIQNFMPEDISVOMLHNEVOLPDARHSTQPRK 60

QY 272 KSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 320
DB 61 KSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 109

RESULT 9

US-08-601-184-2
Sequence 2, Application US/08601184
Patent No. 6043345

GENERAL INFORMATION:

APPLICANT: Zhang, Ke
APPLICANT: Max, Edward E

APPLICANT: Saxon, Andrew
TITLE OF INVENTION: IGE ISOFORMS AND METHODS OF USE
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94114187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,184
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-57950-1/PJS UCLA233-1
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-601-184-2

Query Match 34.0%; Score 581; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 1e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 PRAAEVAFATPEPPGSRDKRTLACLIONFMPEDISVOMLHNEVQLDPARSTTQPKRT 271
DB 1 PRAAEVAFATPEPPGSRDKRTLACLIONFMPEDISVOMLHNEVQLDPARSTTQPKRT 60

QY 272 KSGGFVFSRLVETRAEWEQKDEFICRAVHEAASPSQTVQRAVSNPGK 320
DB 61 KSGGFVFSRLVETRAEWEQKDEFICRAVHEAASPSQTVQRAVSNPGK 109

RESULT 10
US-08-466-163B-1
Sequence 1, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 1
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-08-466-163B-1

Query Match 33.2%; Score 566.5; DB 4; Length 109;
Best Local Similarity 99.1%; Pred. No. 2.5e-47;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 103 DSNPGVSAVLSRPSFDLFIKRSPTITCLVVDLAPSKGTVMLTMSRASGKPVNHSTKRE 162
|||||

DB 1 DSNPGVSAVLSRPSFDLFIKRSPTITCLVVDLAPSKGTVMLTMSRASGKPVNHSTKRE 60

QY 163 EKORNGTLVTSTLPVGTBMDIEGETYOCVTHPHLPALMRSTTKTSGP 212
DB 61 EKORNGTLVTSTLPVGTBMDIEGETYOCVTHPHLPALMRSTTKTSGP 109

RESULT 11
US-08-232-539D-4
Sequence 54, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Ige Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-232-539D-54

Query Match 32.6%; Score 556; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GVSATLSRPSFDLFIKRSPTITCLVVDLAPSKGTVMLTMSRASGKPVNHSTKREKORN 167
DB 1 GVSATLSRPSFDLFIKRSPTITCLVVDLAPSKGTVMLTMSRASGKPVNHSTKREKORN 60

QY 168 GTLVVSTLPVGTBMDIEGETYOCVTHPHLPALMRSTTKTSGP 212
DB 61 GTLVVSTLPVGTBMDIEGETYOCVTHPHLPALMRSTTKTSGP 105

RESULT 12
US-08-464-025A-1
Sequence 1, Application US/08464025A
Patent No. 5994514
GENERAL INFORMATION:
APPLICANT: Jardieu et al.
TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
NUMBER OF SEQUENCES: 27

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/464,025A
;; FILING DATE: 05-Jun-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39,044
;; REFERENCE/DOCKET NUMBER: P0718C3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/952-9881
;; TELEFAX: 650/225-1489
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;;
US-08-464-025A-1
;;
Query Match 30.8%; Score 526; DB 2; Length 119;
Best Local Similarity 90.7%; Pred. No. 2.3e-43;
Matches 107; Conservative 1; Mismatches 2; Indels 8; Gaps 4;
;;
QY 103 DSNPRGVSAVLSRSPDP-LFIRKSPITTCLVVDLAPSKGTVNLTWSRAS---GKPVNHS 158
DB 2 DSNPRGVSAVLSRSPDXLFIRKSPITTCLVVDLAPSKGTVNLTWSRASXKXKPVNHS 61
DB 62 TRREKQRXNXXGTLVTVSTLPGVRDWMIEGTQCRTVHPLRALXMRSTTSGP 119
;;
RESULT 13
US-08-466-151-1
;; Sequence 1, Application US/08466151
;; Patent No. 6037453
;; GENERAL INFORMATION:
;; APPLICANT: Jardiou, Paula M.
;; APPLICANT: Presta, Leonard G.
;; TITLE OF INVENTION: Immunoglobulin Variants
;; NUMBER OF SEQUENCES: 65
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/466,151
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/466163
;; FILING DATE: 06-Jun-1995
;; APPLICATION NUMBER: 08/405617
;; FILING DATE: 15-MAR-1995

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/185899
;; FILING DATE: 26-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/879495
;; FILING DATE: 07-MAY-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/744768
;; FILING DATE: 14-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39,044
;; REFERENCE/DOCKET NUMBER: P0718P2C1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/952-9881
;; TELEFAX: 650/225-1489
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 118 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;;
US-08-466-151-1
;;
Query Match 29.8%; Score 508.5; DB 3; Length 118;
Best Local Similarity 89.8%; Pred. No. 1.1e-41;
Matches 106; Conservative 1; Mismatches 2; Indels 9; Gaps 5;
;;
QY 103 DSNPRGVSAVLSRSPDP-LFIRKSPITTCLVVDLAPSKGTVNLTWSRAS---GKPVNHS 158
DB 2 DSNPRGVSAVLSRSPDXLFIRKSPITTCLVVDLAPSKGTVNLTWSRASXKXKPVNHS 61
DB 159 TRREKQR---NGLIVTSTLPGVRDWMIEGTQCRTVHPLRAL-MRSTTSGP 212
DB 62 TRREKQRXNXXGTLVTVSTLPGVRDWMIEGTQCRTVHPLRALXMRSTTSGP 118
;;
RESULT 14
US-08-646-981-16
;; Sequence 16, Application US/08646981
;; Patent No. 5852183
;; GENERAL INFORMATION:
;; APPLICANT: MAEDA, HIROAKI
;; APPLICANT: EDA, YASUYUKI
;; APPLICANT: KIMACHI, KAZUHIKO
;; APPLICANT: ONO, YOICHI
;; APPLICANT: TOKIYOSHI, SACHIO
;; TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
;; TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
;; STREET: PO BOX 747
;; CITY: FALLS CHURCH
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22040-0747
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,981
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEINER, MARC S
;; REGISTRATION NUMBER: 32,181
;; REFERENCE/DOCKET NUMBER: 1488-106
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 334 amino acids

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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:52:29 ; Search time 32.9929 Seconds
(without alignments)
1657.949 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDKTHTKPPCPAPEL.....HEAASPSQTVQRAVSVPNGK 569

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1766	57.7	428 1 EHHU	Ig epsilon chain C
2	1705.5	55.7	426 1 I36948	Ig epsilon chain C
3	1225	40.0	330 1 GHU	Ig gamma-1 chain C
4	1219	39.8	374 2 S69339	Ig heavy chain Y r
5	1217	39.8	255 4 S31866	Ig gamma-1 chain C
6	1172	38.3	234 2 P0207	Ig gamma chain C r
7	1138	37.2	377 2 A23511	Ig gamma-3 chain C
8	1136	37.1	2 460764	Ig gamma-3 chain C
9	1123	36.7	289 1 G3H0WT	Ig gamma-3 heavy C
10	1107	36.2	326 1 G4HU	Ig gamma-2 chain C
11	1097	35.8	327 1 G4HU	Ig gamma-4 chain C
12	883	28.9	323 1 GHRB	Ig gamma chain C r
13	868.5	28.4	328 2 I47160	Ig gamma 2b chain
14	868.5	28.4	328 2 I47159	Ig gamma 2a chain
15	865	28.3	277 2 I47162	Ig gamma 4 chain C
16	862.5	28.2	429 1 EHRT	Ig epsilon chain C
17	858	28.0	329 1 G2GP	Ig gamma-2 chain C
18	847.5	27.7	328 2 I47158	Ig gamma 1 chain C
19	840.5	27.5	328 2 I47161	Ig gamma 3 chain C
20	834.5	27.3	548 2 S38864	Ig epsilon chain C
21	820	26.8	470 2 S22080	Ig heavy chain pre
22	813	26.6	333 2 P50018	Ig gamma-2b chain
23	812.5	26.6	329 1 G3MSC	Ig gamma-3 chain C
24	811.5	26.5	308 1 G30554	Ig heavy chain C r
25	811.5	26.5	472 2 S31459	Ig gamma-1 chain C
26	801.5	26.2	398 1 G3MSM	Ig gamma-3 chain C
27	794.5	26.0	444 2 P4436	monoclonal antibody
28	789.5	25.8	324 1 G4MS	Ig gamma-1 chain C
29	784.5	25.6	326 2 P50017	Ig gamma-1 chain C

30	784.5	25.6	393 1 G1MSM	Ig gamma-1 chain C
31	776.5	25.4	329 2 S00847	Ig gamma-2c chain
32	776	25.4	330 1 G2MSA	Ig gamma-2a chain
33	776	25.4	469 2 S37483	Ig gamma-2a chain
34	772	25.2	335 1 G2MSAB	Ig gamma-2a chain
35	771	25.2	399 1 G2MSAM	Ig gamma-2a chain
36	766.5	25.0	388 1 EHMS	Ig epsilon chain C
37	761	24.9	446 2 S40295	Ig gamma-2a chain
38	751.5	24.6	474 1 G2MS11	Ig gamma-2b chain
39	750	24.5	423 1 EHMS5	Ig epsilon chain C
40	747.5	24.4	322 2 P50019	Ig gamma-2a chain
41	746.5	24.4	405 1 G2MSBM	Ig gamma-2b chain
42	735	24.0	327 2 S06611	Ig gamma-2 chain C
43	731.5	23.9	475 2 S01321	Ig gamma-2b chain
44	669	21.9	180 2 I46732	Ig gamma heavy cha
45	576	18.8	227 2 PH1215	Ig epsilon chain C

ALIGNMENTS

RESULT 1

EHHU
Ig epsilon chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116;
R:Flanagan, J.C.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region 9
A:Reference number: A22771; MUID:84236029; PMID:6234164
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <FLA>
A:Cross-references: GB:L00022; GB:V00555; NID:g185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseu
A:Reference number: A23195; MUID:84207910; PMID:6327276
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:J00222; NID:g184755
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splic
A:Reference number: PH1214; MUID:92308839; PMID:1613458
A:Accession: PH1214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: EMBL:X63693; GB:S38668; NID:g32987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S
Nucleic Acids Res. 11, 719-726, 1983
A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon
A:Reference number: A93491; MUID:83168897; PMID:6300763
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945; PMID:6288268
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358, 'L', 360-428 <MAX>
A:Cross-references: GB:J00222; NID:g184755
A:Note: This sequence difference may be due to polymorphism
R:Benich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein

A:Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',124
A:Experimental source: myeloma protein Nd
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: B93933
A:Molecule type: mRNA
A:Residues: 1-40:68-114;427-428 <KEN>
A:Cross-references: GB:I00022; NID:g185035
R:Ikemura, S
FEBS Lett. 224, 306-310, 1987
A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment
A:Reference number: S02438; MUID:88083554; PMID:3121387
A:Accession: S02438
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 98-352 <IKE>
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: A53116
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 320-428 <ZH2>
A:Experimental source: myeloma U266-derived cell line AF-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R:Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
A:Reference number: A46536; MUID:93122085; PMID:8419166
A:Accession: C46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-426 <HEL>
A:Cross-references: GB:S5273; NID:g263166; PIDN:AMB24857.1; PID:g263167
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
A:Accession: D46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-391 <HE2>
A:Cross-references: GB:S5276; NID:g263168; PIDN:AMB24858.1; PID:g263169
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
C:Genetics:
A:Gene: GDB:IGHE
A:Cross-references: GDB:119335; OMIM:147180
A:Map position: 14q32.33-14q32.33
A:Introns: 1/1; 104/1; 211/1; 319/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 14
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
F:22-87/Domain: immunoglobulin homology <IM1>
F:128-195/Domain: immunoglobulin homology <IM2>
F:232-301/Domain: immunoglobulin homology <IM3>
F:338-407/Domain: immunoglobulin homology <IM4>
F:14Disulfide bonds: Interchain (to light chain) bonds: #status predicted
F:15-109,29-85,133-193,345-405/Disulfide bonds: #status predicted
F:21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:121,209/Disulfide bonds: Interchain (to heavy chain) #status predicted

```

Matches 347: Conservative 17; Mismatches 57; Indels 24; Gaps 7;
OY 129 REPQYITTPERDELTKNOVSLT--CLVKGYPYSDIAVENESNQPENNYKTP-PLYDS 185
Db 4 QSPSVPFLTRCCKKIPSNATSVTLGCLATGFPEPVVMTWT-GLNCTMTLPAFTLL 62
OY 186 VGSEFLYSKILVDRSKRMQGVNFCGSYVHEALHNHY-QORSLSLSPKVEEGSGSGGS 244
Db 63 SGHATISLTLV-SGAMAK-QMFTCRVANHPTSSIDWDNKNFFSYC----- 105
OY 245 GGGGSFTPPYKILIOSSCDGGGHPPTIQLCLVSGYTPGTINTIMLEDGVMDVLDSTA 304
Db 106 --SRDFTPPYKILIOSSCDGGGHPPTIQLCLVSGYTPGTINTIMLEDGVMDVLDSTA 163
OY 305 STTQEGELASTQSELTLSQKHWLSDRYTCQVYVQGHFFEDSTKCADSNRGYSAYLSR 364
Db 164 STTQEGELASTQSELTLSQKHWLSDRYTCQVYVQGHFFEDSTKCADSNRGYSAYLSR 223
OY 365 PSPDPLFRKSPPTTCLVLDLAPSKGYVNLTWMSRASGKPVNHSRKEEKORNGTLTVYST 424
Db 224 PSPDPLFRKSPPTTCLVLDLAPSKGYVNLTWMSRASGKPVNHSRKEEKORNGTLTVYST 283
OY 425 LPVGRMDIESETQCRVTHPHLRALMRSTTKSGPRAAEVYAFAPEMPGRSDKRTL 484
Db 284 LPVGRMDIESETQCRVTHPHLRALMRSTTKSGPRAAEVYAFAPEMPGRSDKRTL 343
OY 485 ACLIQNFWPEDIYQWMLNEVOLFDPARSTQPRKTKSGGFVFSRLVETFAEMQKDEF 544
Db 344 ACLIQNFWPEDIYQWMLNEVOLFDPARSTQPRKTKSGGFVFSRLVETFAEMQKDEF 403
OY 545 ICRVHFAASPSQTVQRAVSYNPGK 569
Db 404 ICRVHFAASPSQTVQRAVSYNPGK 428

RESULT 2
136948
Ig epsilon-chain - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C:Accession: J36948
R:Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang
A:Reference numbers: J36948; MUID:87147196; PMID:3103123
A:Accession: J36948
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-426 <RES>
A:Cross-references: GB:M15398; NID:g176797; PIDN:AAA5416.1; PID:g176798
C:Genetics:
A:Introns: 103/1; 209/1; 317/1
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
F:J36-405/Domain: immunoglobulin homology <IM>

Query Match 55.7%; Score 1705.5; DB 2; Length 426;
Best Local Similarity 76.0%; Pred. No.1.3e-98;
Matches 338; Conservative 20; Mismatches 62; Indels 25; Gaps 8;
OY 129 REPQYITTPERDELTKNOVSLT--CLVKGYPYSDIAVENESNQPENNYKTP-PLYDS 185
Db 3 RSPSLFPLTRCCKKIPSNATSVTLGCLAMGYFPEPVMTWDA-GLNCTMTLPAFTLLTP 61
OY 186 VGSEFLYSKILVDRSKRMQGVNFCGSYVHEALHNHY-QORSLSLSPKVEEGSGSGGS 244
Db 62 SGHATISLTLV-SGAMAK-QMFTCRVANHPTSSIDWDNKNFFSYC----- 104
OY 245 GGGGSFTPPYKILIOSSCDGGGHPPTIQLCLVSGYTPGTINTIMLEDGVMDVLDSTA 304
Db 105 --SRDFT-PTVKVLIQSSCDGGGHPPTIQLCLVSGYTPGTINTIMLEDGVMDVLDSTA 161
OY 305 STTQEGELASTQSELTLSQKHWLSDRYTCQVYVQGHFFEDSTKCADSNRGYSAYLSR 364
Db 164 STTQEGELASTQSELTLSQKHWLSDRYTCQVYVQGHFFEDSTKCADSNRGYSAYLSR 223

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Db 162 SATQEGELASTQSELTLSSOKHMLSDRTYTCQVTVYQSGTFEDSTFKCADSNRGVSAVLSR 221
Oy 365 PSEPDLFIRKSPITTCVLVDLPAPSKGTVNLTWASRSGKPVNHSRKEKORNGTLTVST 424
Db 222 PSEPDLFIRKSPITTCVLVDLPAPSKGTVNLTWASRSGKPVNHSRKEKORNGTLTVST 281
Oy 425 LPVGTDMIGETVYQCVHTPHLPRLALMRSTTKSGPRAAEVAFATPEWGSRDRTL 484
Db 282 LPVGTDMIGETVYQCVHTPHLPRLALMRSTTKSGPRAAEVAFATPEWGSRDRTL 341
Oy 485 ACLIQNPEDISVQWLNHEVQLPDARHSTTPPKTKSGFVFVSRLAEVRAEWDQDEF 544
Db 342 ACLIQNPEDISVQWLNHEVQLPDARHSTTPPKTKSGFVFVSRLAEVRAEWDQDEF 401
Oy 545 ICRVHEAASPQTVORAVSNPGR 569
Db 402 ICRVHEAASPQTVORAVSNPGR 426

RESULT 3
IGHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <EID>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the Gln(17) allelotypic marker, 97-Lys, and the Gln(1) markers, R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obara, M.; Nixaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113/235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Accession: B90563
A:Molecule type: Protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Accession: B90564
A:Molecule type: Protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Postlitz, H.; Hilschmann, N.
Hoppe-Seilyer's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475

A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: Protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A:Note: This sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seilyer's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL, disulfide bonds
A:Accession: A91723
A:Molecule type: Protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seilyer's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog
endriamide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/L: 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 40.0%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. NO. 6.3e-69;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EPKSCDKTHGPCPCAPRLGPGSVFLFPKPKDTLMSRPETVCVVVDVSHEDPEYKF 60
Db 99 EPKSCDKTHGPCPCAPRLGPGSVFLFPKPKDTLMSRPETVCVVVDVSHEDPEYKF 158
Oy 61 NMVYDGVVHVWVKTRPREQYNSYRVSYSYLVTHQMMNGKRYCKVSNKALAPRIEKT 120
Db 159 NMVYDGVVHVWVKTRPREQYNSYRVSYSYLVTHQMMNGKRYCKVSNKALAPRIEKT 218
Oy 121 ISKAKVQPREQVYVTLPPSRDELTKNQSLTCLVKGFPYSDIAVEMESNGCPENNYKTP 180
Db 219 ISKAKGQPREQVYVTLPPSRDELTKNQSLTCLVKGFPYSDIAVEMESNGCPENNYKTP 278
Oy 181 PVLDSVGSFELYSKLTVDKSRMQGCVNSVCSYMHGALHNHYQQRSLSPGK 232
Db 279 PVLDSVGSFELYSKLTVDKSRMQGCVNSVCSYMHGALHNHYQQRSLSPGK 330

RESULT 4
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilchi, A.A.; Aucoeur, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049

A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamlich, A.A.
Submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: Immunoglobulin C region; immunoglobulin homology

Query Match 39.8%; Score 1219; DB 2; Length 374;
Best Local Similarity 96.1%; Pred. No. 1,7e-68;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 143 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 202
QY 61 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMWMNGKEKCKVSKALPAPIEKT 120
DB 203 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMWMNGKEKCKVSKALPAPIEKT 262
QY 121 ISKAKVQPREPOVYTLPPSDELTKNOVSLTCLVKGYPSDIAVEMWNSQPENNYKTP 180
DB 263 ISKAKGPREPOVYTLPPSDEMTKNOVSLTCLVKGYPSDIAVEMWNSQPENNYKTP 322
QY 181 PVLDSDGSFFLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYTKSLSLSPGK 232
DB 323 PVLDSDGSFFLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYTKSLSLSPGK 374

RESULT 5
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in *Escherichia coli*
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
Submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: Immunoglobulin
F:1-22/Region: *Escherichia coli* outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 39.8%; Score 1217; DB 4; Length 255;
Best Local Similarity 96.6%; Pred. No. 1,4e-68;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 24 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 83
QY 61 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMWMNGKEKCKVSKALPAPIEKT 120
DB 84 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMWMNGKEKCKVSKALPAPIEKT 143
QY 121 ISKAKVQPREPOVYTLPPSDELTKNOVSLTCLVKGYPSDIAVEMWNSQPENNYKTP 180
DB 144 ISKAKGPREPOVYTLPPSDELTKNQVSLTCLVKGYPSDIAVEMWNSQPENNYKTP 203
QY 181 PVLDSDGSFFLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYTKSLSLSPGK 232

DB 204 PVLDSDGSFFLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYTKSLSLSPGK 255

RESULT 6
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Enllich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 1172; DB 2; Length 234;
Best Local Similarity 95.6%; Pred. No. 8e-66;
Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 10 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 69
QY 61 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMWMNGKEKCKVSKALPAPIEKT 120
DB 70 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMWMNGKEKCKVSKALPAPIEKT 129
QY 121 ISKAKVQPREPOVYTLPPSDELTKNOVSLTCLVKGYPSDIAVEMWNSQPENNYKTP 180
DB 130 ISKAKGPREPOVYTLPPSDELTKNQVSLTCLVKGYPSDIAVEMWNSQPENNYKTP 189
QY 181 PVLDSDGSFFLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYTKS 225
DB 190 PVLDSDGSFFLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYTKS 234

RESULT 7
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene.
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGH3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Initons: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 37.2%; Score 1138; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 1,9e-63;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 146 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKF 205
QY 61 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMWMNGKEKCKVSKALPAPIEKT 120


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Db      206 KMYVDGVEVHNAAKTRPREQYNSTFRVSVLTVLHODLNKEKCKVSNALPAPIKRT 265
      121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
      266 ISKTRKGQPREPOVYTLPPSRDEMTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 325
Qy      181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPGK 232
      326 PVLDSGSGFFLYSKLTVDKSRWQGNLFSCVMEHALHNHRTQKSLSPGK 377

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RESULT 8

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A: gamma-3 chain C region, form IAT - human
A:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Letfranc, G.; Letfranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <ITM>

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Query Match      37.1%; Score 1136; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 2.5e-63;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy      1 EPKSCDTHTCPPCPAPRLGSPVFLFPKPKDTLMSRPEVTCVAVDVSHEDPEVKF 60
      146 EPKSCDTPPPCPAPRLGSPVFLFPKPKDTLMSRPEVTCVAVDVSHEDPEVKF 205
Qy      61 NMWYDGVVHNAAKTRPREQYNSTFRVSVLTVLHODLNKEKCKVSNALPAPIKRT 120
      206 KMYVDGVEVHNAAKTRPREQYNSTFRVSVLTVLHODLNKEKCKVSNALPAPIKRT 265
Db      121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
      266 ISKTRKGQPREPOVYTLPPSRDEMTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 325
Qy      181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPGK 232
      326 PVLDSGSGFFLYSKLTVDKSRWQGNLFSCVMEHALHNHRTQKSLSPGK 377

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RESULT 9

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G3HWTI
A: gamma-3 heavy chain disease proteins - human
A:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-
A:Reference number: A90442; MUID:81021548; PMID:6774747
A:Contents: heavy chain disease protein W15
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
A>Note: The molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A>Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cc
A>Note: the sequence of residues 42-76 was taken from the reference that follows
R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A:Reference number: A92219; MUID:77118561; PMID:403263
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W

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A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MTC>
A>Note: the hinge region in gamma-3 chains is about four times as long as in other ga
      lue segment (12-28)
A>Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in
      R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
      Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of t
      A:Reference number: A90198; MUID:77021516; PMID:823945
A:Contents: heavy chain disease protein ZUC, partial sequence corresponding to residu
      A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A>Note: this protein lacks most of the V region, all of the CH1 region, and part of t
      R:Alexander, A.; Steimetz, M.; Barilauf, D.; Frangione, B.; Franklin, E.C.; Hood,
      Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti
      A:Reference number: A93915; MUID:82247835; PMID:6808505
A:Contents: heavy chain disease protein Omn
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-
A:Note: a carboxyl-terminal Lys is removed posttranslationally
A:Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein W15 is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339, OMTM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglytamic acid
F:203-270/Domain: immunoglobulin homology <ITM>
F:140/Binding site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6,140/Binding site: carbonylurate (Asn) (covalent) #status experimental

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Query Match      36.7%; Score 1123; DB 1; Length 289;
Best Local Similarity 88.3%; Pred. No. 1.1e-62;
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy      1 EPKSCDTHTCPPCPAPRLGSPVFLFPKPKDTLMSRPEVTCVAVDVSHEDPEVKF 60
      59 EPKSCDTPPPCPAPRLGSPVFLFPKPKDTLMSRPEVTCVAVDVSHEDPEVKF 118
Db      61 NMWYDGVVHNAAKTRPREQYNSTFRVSVLTVLHODLNKEKCKVSNALPAPIKRT 120
      119 KMYVDGVEVHNAAKTRPREQYNSTFRVSVLTVLHODLNKEKCKVSNALPAPIKRT 178
Qy      121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
      179 ISKTRKGQPREPOVYTLPPSRDEMTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 238
Db      181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPG 231
      239 PVLDSGSGFFLYSKLTVDKSRWQGNLFSCVMEHALHNHRTQKSLSPG 289

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RESULT 10

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G2HU
A: gamma-2 chain C region - human
A:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

```



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A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplo
A:Reference number: A91749; MUID:64030930; PMID:613520
A:Accession: A91749
A:Molecule type: mRNA
A:Residues: 1-323 <BERR>
A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R:Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobul
A:Reference number: A90290; MUID:76135469; PMID:1243651
A:Accession: A90290
A:Molecule type: protein
A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>
R:Matens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A:Title: Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain
A:Reference number: A93928; MUID:83299917; PMID:6193512
A:Accession: A93928
A:Molecule type: mRNA
A:Residues: 88-103, 'W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A:Cross-references: GB:M6426; NID:g16511; PID:AAA31289.1; PID:g165112
A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker
R:Frutcher, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
A:Reference number: A90245; MUID:70110015; PMID:5461106
A:Accession: A90245
A:Molecule type: protein
A:Residues: 132-143, 'E', 145-161 <FRU>
R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A:Reference number: A94416
A:Accession: A94416
A:Molecule type: protein
A:Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',
A:Note: this has the e15 allotypic marker, 185-Ala
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into Ia
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-82/Domain: immunoglobulin homology <IM1>
F:130-199/Domain: immunoglobulin homology <IM2>
F:236-303/Domain: immunoglobulin homology <IM3>
F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      28.9%; Score 883; DB 1; Length 323;
Best Local Similarity 64.5%; Pred. No. 1e-47;
Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

QY      1 EPKSCDKTH-----TC-PPCDAPELLGSPVLEPPPKKDTLMSRPEV 44
      : : : : :      : : : : :
DB      76 QPVCNVNHPATNTKVDKTVAPSTCSKPTCPPELLGSPVFIEPPKPKDTLMSRPEV 135
QY      45 TCVVVDVSHDEPEKFNMYVDGVEYHNKTKTPREDOYNSTRVSVLTVLHQNMMNGKEY 104
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      136 TCVVVDVSDDEPEQVFTWYINNEQVRTAARPLRDOQFSTRIRVYSTPLTHQDWLRKEF 195
QY      105 KCKVSNKALPAPIETITISKAKVOPREPOVYTLPPSRDLTLKNQVSLTCLVNGFYPSDIAY 164
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      196 KCKHNKALPAPIETITISKARGQPLERPKYVITMGPPRRELSSRSVSLTCMINGFTPSDISV 255
QY      165 EWSNGQENNYKTTTPVYLDSVGSFFLYSLKTVLDSKSRMGOQNVGSCVMEBALHNHYQOR 224
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      256 EWEKNGKADENYKTTTPAVLSDGSYFLYLNKLSVPTSEMQRDQVFTCSVMEDALHNHYQK 315
QY      225 SLSLSPGK 232
      : : : : :
DB      316 SISRSPGK 323

```

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:47:19 ; Search time 17.7654 Seconds

(without alignments)
1328.428 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKHTPCPEAPELL.....HEAASPSQTVGRASVNPCK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1766	57.7	428	1	EPC_HUMAN
2	1225	40.0	330	1	GCI_HUMAN
3	1128	36.9	290	1	GCI_HUMAN
4	1107	36.2	326	1	GCI_HUMAN
5	1097	35.8	327	1	GCI_HUMAN
6	883	28.9	323	1	GCI_HUMAN
7	862.5	28.2	429	1	EPC_RAT
8	858	28.0	329	1	GCI_HUMAN
9	826	27.0	421	1	EPC_MOUSE
10	813	26.6	333	1	GCI_MOUSE
11	812.5	26.6	329	1	GCI_MOUSE
12	801.5	26.2	398	1	GCI_MOUSE
13	789.5	25.8	324	1	GCI_MOUSE
14	784.5	25.6	393	1	GCI_MOUSE
15	784.5	25.6	329	1	GCI_MOUSE
16	776.5	25.4	329	1	GCI_MOUSE
17	776	25.4	330	1	GCI_MOUSE
18	776	25.2	335	1	GCI_MOUSE
19	771	25.2	399	1	GCI_MOUSE
20	751.5	24.6	336	1	GCI_MOUSE
21	747.5	24.4	322	1	GCI_MOUSE
22	746.5	24.4	405	1	GCI_MOUSE
23	488.5	16.0	455	1	GCI_MOUSE
24	479.5	15.7	476	1	GCI_MOUSE
25	463.5	15.1	454	1	GCI_MOUSE
26	461	15.1	458	1	GCI_MOUSE
27	452	14.8	479	1	GCI_MOUSE
28	443.5	14.5	457	1	GCI_MOUSE
29	436.5	14.3	454	1	GCI_MOUSE
30	427	14.0	450	1	GCI_MOUSE
31	410	13.4	391	1	GCI_MOUSE
32	391	12.8	438	1	GCI_MOUSE
33	382	12.5	461	1	GCI_MOUSE

34	373	12.2	438	1	HVC2_HETFR
35	355	11.6	446	1	MUC_CHICK
36	347	11.3	340	1	ALC2_HUMAN
37	339.5	11.1	393	1	HVC3_HETFR
38	334.5	10.9	353	1	ALC1_HUMAN
39	326	10.7	353	1	ALC1_HUMAN
40	308	10.1	370	1	ALC1_HUMAN
41	303	9.9	344	1	ALC1_HUMAN
42	293.5	9.6	299	1	ALC1_HUMAN
43	254	8.3	481	1	MUC_MOUSE
44	229	7.3	383	1	DTC_HUMAN
45	179	5.8	1242	1	NPHN_MOUSE

ALIGNMENTS

RESULT 1

EPC_HUMAN

ID EPC_HUMAN STANDARD; PRT; 428 AA.

AC P01854:

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE I9 epsilon chain C region.

GN IGHE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83168897; PubMed=6300763;

RA Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K., Kikuchi M., Sugino Y., Nishida Y., Honjo T.;

RT "Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon chain cDNA."

RL Nucleic Acids Res. 11:719-726(1983).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANT LEU-359.

RX MEDLINE=83001945; PubMed=6288268;

RA Max E.E., Batley J., Ney R., Kirsch I.R., Leder P.;

RT "Duplication and deletion in the human immunoglobulin epsilon genes."

RL Cell 29:691-699(1982).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=84236029; PubMed=6234164;

RA Flanagan J.G., Rabbits T.H.;

RT "The sequence of a human immunoglobulin epsilon heavy chain constant region gene, and evidence for three non-allelic genes."

RL EMBO J. 1:655-660(1982).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=84207910; PubMed=6327276;

RA Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;

RT "Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene that lacks introns."

RL EMBO J. 1:1539-1544(1982).

RN [5]

RP PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).

RA Benlich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;

RT (In) Bach M.K. (eds.);

RL Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978).

RN [6]

RP SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.

RX MEDLINE=83065234; PubMed=6815656;

RA Kenen J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.;

RT "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."

RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).

RN [7]

Query Match	Best Local Similarity	Score 1766;	DB 1;	Length 428;
Matches 347;	Conservative 17;	Mismatches 57;	Indels 24;	Gaps 7;
129	REPQVYTLPPSRDELTKNOVSLT	-CLVKGFP	SDIAV	EWESNGOPENNYKTPP-PYLD
186	VGSFFLYSKLVDSKRWQGVSCVYHNEHLMHNY	-QQNSLS	SPKRV	GGSGGGSGGGS 244
63	SGHATITSLTVL-SGANAK	-OMFCRAV	HPSS	STDWVNDKNTFYSVC----- 105
245	GGGGSFPPTWYKLIQSSCDGGGHPPTIOLCLVSGTPTG	INTL	TWLEDG	GVMDVLDSTA 304
106	--SDFTPFPYKLIQSSCDGGGHPPTIOLCLVSGTPTG	INTL	TWLEDG	GVMDVLDSTA 163
305	STTQEGELASTQSELTLQKHMVLSDRYTQCVITQVQGT	FEDSTK	KCADSN	PRGVSAVLSR 364
164	STTQEGELASTQSELTLQKHMVLSDRYTQCVITQVQGT	FEDSTK	KCADSN	PRGVSAVLSR 223
365	PSPPDLIRKSPITTLCLVVDLAPSKGVNLTWSASGKPVNH	STRKEK	ORNGT	TLVTYST 424
224	PSPPDLIRKSPITTLCLVVDLAPSKGVNLTWSASGKPVNH	STRKEK	ORNGT	TLVTYST 283
425	LPVSTRMIEBETVQCVTHNHLRALMRSTTKSGRAAEVYAFAT	PREP	SGRDK	RTL 484

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Db      284 LPVGRDWTLEGETYQC R VTHPHPLRALMNSTRTSGSPRAAPEYYATAPEMPQSRKRTL 343
Oy      465 ACTIONEMEDISVGMHLNHEVOLPDARHSTTOPRKTKGSEFFVSRLRYTRAMEOKDER 544
         |||||||
Db      344 ACTIONEMEDISVGMHLNHEVOLPDARHSTTOPRKTKGSGFFVSRLRYTRAMEOKDER 403
Oy      545 ICRVAHEAASPQTQVORAHSVNGK 569
         . |||||||
Db      404 ICRVAHEAASPQTQVORAHSVNGK 428

RESULT 2
GCL_HUMAN
AC ID GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human)..
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin, VII. Amino
RL acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RN Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RL acid sequence of heavy-chain cyanogen bromide fragments H3-H7.";
RN Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponsstngl H., Hilschmann N.;
RT "The role of antibody structure. The primary structure of a
RL monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RL peptides and discussion of the complete structure.";
RN Hope-seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL). AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RN Hope-seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL intrachain disulfide bonds.";
RN Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreier L., Schwarz J., Reichel W., Hilschmann N.;

```

"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the RT cyanoen bromide cleavage products, and the disulfide bridges.," RT Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
[8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; Pubmed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.,"
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198,267&272.

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DR EMBL: J00228; AAC82527.1; ALT_INT.
DR PIR: A02146; GHHD.
DR PDB: 1FC1; 15-JUL-92.
DR PDB: 1FC2; 15-JUL-92.
DR Genew: HGNC:5525; IGHL1.
DR MIM: 147100; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; IGCL; 2.
DR PROSITE: PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 3D-structure.
KW 3D-structure.
FT 1 1
FT NON_TER 1 98
FT DOMAIN 1 98
FT 99 110
FT DOMAIN 111 223
FT 224 330
FT DOMAIN 224 330
FT DISULFID 27 83
FT DISULFID 103 103
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT 239 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166

FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770BE106C2FA33D CRC64;
Query Match 40.0%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.2e-77;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDTHHCPCPAPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 60
DB 99 EPKSCDTHHCPCPAPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 158
QY 61 NWYDGYEVHNAKTKPREDOYNSTYRVVSVLTVLHQMNMGKEYCKKVSNAKLPAPLEKT 120
DB 159 NWYDGYEVHNAKTKPREDOYNSTYRVVSVLTVLHQDMLNGKEYCKKVSNAKLPAPLEKT 218
QY 121 ISRAKQVPRPQVYTLPPSBDLTKNOVSLTCLVKGFPSPDIAYEMSNQPENNYKTP 180
DB 219 ISRAKQVPRPQVYTLPPSBDLTKNOVSLTCLVKGFPSPDIAYEMSNQPENNYKTP 278
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNFSCVYMHGALHNHYOQKSLSPGK 232
DB 279 PVLDSVGSFPLYSKLTVDKSRWQGNFSCVYMHGALHNHYOQKSLSPGK 330
RESULT 3
GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=81021548; Pubmed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL Biochemistry 19:4304-4308(1980).
[2]
RN REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; Pubmed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RT quadruplication of a 15-amino acid residue basic unit.,"

RA Krawinkel U., Rabbits T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 RT genes";
 RL EMBO J. 1:403-407(1982).
 RN (4)
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 RT evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN (5)
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RT domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN (6)
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN (7)
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN (8)
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RT immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN (9)
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RL "Disulphide bridges of the heavy chain of human immunoglobulin G2";
 RL Biochem. J. 121:217-225(1971).
 RN (10)
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 CC -----
 CC EMBL: J00230; AAB59393.1; -
 DR PIR: A02148; G2HD.
 DR HSSP: P01857; 1FC1.
 DR Genew: HGNC:5526; IGHG2.
 DR MIM: 147110; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; IGCL; 2.
 DR PROSITE: PS00290; IG_MHC; 2.
 KM Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109
 FT SEQUENCE 326 AA; 35884 MW; 8310878C687BCF9C CRC64;
 SQ
 Query Match 36.2%; Score 1107; DB 1; Length 326;
 Best Local Similarity 88.4%; Pred. No. 2.9e-69;
 Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;
 OY 1 EPKSCDKTHICTPCPCAPRLGGSVFLEPPKPKDTLMISRPPEVTCVVDVSHEDPEYKF 60
 DB 99 ERKCCVE---CPGPCPAPV-VAGPSVFLEPPKPKDTLMISRPPEVTCVVDVSHEDPEYQF 154
 OY 61 NMVYDGVGVHNAKTKPREQNSYFRVSVLTFLVHONMNGEKYCKRKNAALPAPTEKT 120
 DB 155 NMVYDGVGVHNAKTKPREQNSYFRVSVLTFLVHONMNGEKYCKRKNAALPAPTEKT 214
 OY 121 ISKAKVQPREPOVYTLPPSPDELTKNQVSLTCLVKGFYPSDIAVEMESGPOENNYKTP 180
 DB 215 ISKTKGQPREPOVYTLPPSPDELTKNQVSLTCLVKGFYPSDIAVEMESGPOENNYKTP 274
 OY 181 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMHEDALNNHYQKSLSPCK 232
 DB 275 PMLDSGSGSFELYSKLTVDKSRWQGNVFSQVMHEDALNNHYQKSLSPCK 326
 RESULT 5
 G4_HUMAN STANDARD: PRT: 327 AA.
 ID G4_HUMAN
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Ig gamma-4 chain C region.
 DE IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid:9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene";
 RL DNA 1:11-18(1981).
 RN (2)
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RT constant region of a gamma 4 chain";
 RL Biochem. J. 117:33-47(1970).
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QY 105 KCVSNKALPAPIRKTSKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYPSPDIIV 164
 Db 196 KCKVHNKALPAPIRKTSKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYPSPDIIV 255
 QY 165 EMENSGPENNKTTPVLDVSGSFLLSKITVDKSRNOCNVSCSYMHALNHVYQOR 224
 Db 256 EMEKNGAEADYKTTTPALVDSGDSYFLYNKLSVPTSEWNGDVFTCSYMHALNHVYQOR 315
 QY 225 SLSPGK 232
 Db 316 SISRSPGK 323

RESULT 7

EPC_RAT STANDARD: PRT: 429 AA.

AC P01855: 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig epsilon chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
 RC STRAIN=10U/C/NSL;
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Petersson U., Engstrom A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E.";
 RL Nucleic Acids Res. 10:6041-6049(1982).

RN [2]
 RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
 RX MEDLINE=83182019; PubMed=6820340;
 RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
 RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
 RT construction, identification, and DNA sequence.";
 RL DNA 1:335-343(1982).

RN [3]
 RP SEQUENCE OF 205-306 FROM N.A.
 RX MEDLINE=82174576; PubMed=6803238;
 RA Hellman L., Petersson U., Bennich H.;
 RT "Characterization and molecular cloning of the mRNA for the heavy
 RT (epsilon) chain of rat immunoglobulin E.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).

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 CC -----

DR EMBL: J00744; AAA41379.1; ALT_INIT.

DR PIR: A02143; EHRT.

DR HSSP: P01854; IIGC.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003597; Ig_C1.

DR InterPro: IPR003600; Ig_Like.

DR Pfam: PF00047; Ig_4.

DR SMART: SM00410; Ig_Like; 3.

DR PROSITE: PS00290; Ig_MHC; 3.

KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT CONFLICT 168 168 R -> N (IN REF. 2).
 FT CONFLICT 308 308 P -> L (IN REF. 2).
 SQ SEQUENCE 429 AA; 48671 MW; D2970B34EF8A2B0 CRC64;

Query Match 28.2%; Score 862.5; DB 1; Length 429.

Best Local Similarity 40.5%; Pred. No. 2.8e-52;
 Matches 181; Conservative 71; Mismatches 162; Indels 33; Gaps 11;

QY 126 VQPREPOVYTLPPSRDELTKNQVSLTCLVKGYPSPDIIVEMENSGPENNKTTPVLDV 185
 Db 1 VSVKAPSLYPLKPPSSENTAS-VTLGCLVKYFPDPVTVVYS-----DSLNTSTMPSS 54
 QY 186 VGSFELSKITVDKSRNOCNVSCSYMHALNHVYQORSLSPCKVEGGSGSGGS 244
 Db 55 IGSGL--KTTISQMTSMKSAKNFTCHTH-APSTFVSDLITRRAPVNI----- 100
 QY 245 GGGGSFTPPVTKIQQSCDGGGHPPTQLCLVSGYPTGTTITWL-EDGQVMDVLIST 303
 Db 101 -----TKPTVDLHSSCDPNA-FHSTQLCYFYGHIONDVSIHMLMDRKRIVETHAQN 153
 QY 304 ASTQOEGLASTOSEELTSQKHWLSDRKYTOOVYVYOGFTFEDSRKKCADSNPRVSATLS 363
 Db 154 VLKEEGKLASTYSLRLNTQQQWMSSEFTCKVTSQGENYVAHTRRCSDDEPRGVITYLI 213
 QY 364 RSPFDLFRKSPRTTCLVLDLAPSKGVNLTWASRASKPVNHSTRKEKORNGTLVTS 423
 Db 214 PPSPLDLYENGTPKLITCLVLDL-ESEENITVTVWREKKSIGSASORSTKHNMTTITS 272
 QY 424 TLPGSTRWIGETVYQCRVTHPLPALMSTTSTGPRAADEVYAFATPMPGSRDKRT 483
 Db 273 ILPVDKDWIGEGYQCRVHDHPHPKPIVRSITKAPKRSAPDEVYVFLPPE-EEEKDKRT 331
 QY 484 LACTIOMFMPDISVOWLHNEVQLPDAHSTTORPKTKSGS--FVFSRLVTAEMRQK 541
 Db 332 LTCLIQNEFPDISVOWLQDSKLLPKSHOSTTTPKLYGNSQRFIFSRLEVTAALMTOT 391
 QY 542 DEICRAVHEAASPSQTVQRAVSVPNG 568
 Db 392 KQFTCRVTHEALRERKLERITKSLG 418

RESULT 8

GC2_CAVPO STANDARD: PRT: 329 AA.

AC P01862: 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-2 chain C region.
 OS Cavia porcellus (Guinea pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.

OC NCBI_TaxID=10141;
 OX [1]
 RP SEQUENCE OF 1-3.
 RA Trischmann T.M.;
 RL Submitted (Apr-1975) to the PIR data bank.

RN [2]
 RP SEQUENCE OF 4-68.
 RX MEDLINE=71058471; PubMed=5538606;
 RA Birtheim B.K., Hussain Q.Z., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin G(2). 3. Amino acid sequence of the region around the
 RT half-cystine joining heavy and light chains.";
 RL Biochemistry 10:18-25(1971).

RN [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RX MEDLINE=71058486; PubMed=5538616;
 RA Turner K.J., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin G(2). II. Amino acid sequence of the carboxyl-terminal
 RT and hinge region cyanogen bromide fragments.";
 RL Biochemistry 10:9-17(1971).

RN [4]
 RP SEQUENCE OF 134-226.
 RX MEDLINE=75036072; PubMed=4429665;
 RA Tracey D.E., Cebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2

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RT antibodies."
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies."
RL Biochemistry 13:4804-4811(1974).
RN [6]
RX DISULFIDE BONDS.
RP MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamu M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR: A02151; G2GP.
DR HSSP: P01842; 7EAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; Igcl; 2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 28.0%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No. 4,1e-52;
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

QY 1 EPKSCDKTHTCPAPAEELLCGSPVFLPPPKRDTLMSRTPEVTCVAVDVSHEDEPKF 60
DB 101 ZPBRG----TCPKRPPRNLGGPSVFTPRPKDTLMSLTPRTCVAVDVSODEPEYOF 156
QY 61 NWYDVEVHNVKTRPREQYNSYRVVSVLTLHNMNGKEXKCKVSNKALPAPIEKT 120
DB 157 TWFDNKPVGNAETKRPVEQYNTFRVESVLPIDHODWLRGKEFKCKYNNKALPAPIEKT 216
QY 121 ISKAKVQPREQVYTLTPSRDELTKNOVSLTCLYKGFPSDIAVEMESNGQP--ENNYKT 178
DB 217 ISKTKGAPRMPDYVTLTPSRDELTKSKVSYTCLINFPADIHVEMSNRPVSEKEKYN 276
QY 179 TPPLVDVSGSPFLSKLTVDKSRWMOGQNVFSCSVMEHLNHNHYOORSLSLSPG 231
DB 277 TPPIEDADGSLFKLTVDKSNANDOGIVYTCSVMHEHLNHNHYOORSLSRSPG 329

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RX MEDLINE=84236092; PubMed=6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RT comparison with the human epsilon gene sequence."
RL EMBO J. 1:1117-1123(1982).
RN [2]
RP REVISIONS.
RA Honjo T.;
RL Submitted (Apr-1986) to the EMBL/Genbank/DBJ databases.
RX SEQUENCE OF 34-421 FROM N.A.
RP MEDLINE=83117774; PubMed=6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
RT chain cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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CC -----
DR EMBL: X01857; CAA25977.1;
DR EMBL: X01857; CAA25978.1;
DR PIR: A02145; EHMS.
DR PIR: A02144; EHMS.
DR HSSP: P01854; 11GE.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00410; Ig-like; 2.
DR SMART: SM00407; Igcl; 2.
DR PROSITE: PS00290; Ig_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.
FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 BY SIMILARITY.
FT DISULFID 121 180 BY SIMILARITY.
FT DISULFID 226 285 BY SIMILARITY.
FT DISULFID 330 392 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 421 AA; 47320 MW; 8F909E1F30A06B47 CRC64;

Query Match 27.0%; Score 826; DB 1; Length 421;
Best Local Similarity 39.4%; Pred. No. 9e-50;
Matches 176; Conservative 80; Mismatches 149; Indels 42; Gaps 11;

QY 129 REPQVYTLTPSRDELTKNOVSLTCLYKGFPSDIAVEMESNGQENNYKTPPYLDSVGS 188
DB 3 RNPGLVPLPKPKCKGAS---MTLGLCTVDYFPNPTVWYSLSL-----MSIVNF 49
QY 189 FFLYSKLTVDKSR---W-QQGNVSCSVMEHLNHNHYOORSLSLSPKVEGGSGGGGS 244
DB 50 PALGSELKVTTSQVTSWGSKAKNFTCHVTHPPSFN--ESRILIVRPNI----- 96
QY 245 GGGSGFTPPYKVIQSSCDGGGHPPTIOLCLVSGTPTGINTITWL-EDGQVMDVLDST 303
DB 97 -----TEPTIELLHSSCDRNA-FHSITQLCYFTYGHILNDVSVSWIMDREITDYLAQT 149

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QY 304 ASTOGEELASTOSELTLQKHLMSDRYTCQVYOGHTFEDSTKRCADSNPRGVSAYLS 363
Db 150 VLKEEGELASTGCKLNTTEQOMMSSEFTCKVTSQGVLYLAHRRCPDHPRGVITLYLI 209
QY 364 RPSFDFLIRKSPITTLVLDLADPSKGVNLTWBSRASKPVNHNSTRKEKORNGTLVTS 423
Db 210 PPSPLDLYQNGAPKLTCLVLDLESEK - NVNVTWNQEKTSVSASQWYTKHNNMTTTSITS 268
QY 424 TLPGTRDMIGETVYOCVPHPLPRLMNSTKTSGRAPAEVAFATPEMPSRDKRT 483
Db 269 ILPVAKDMIGETVYOCVPHPLPRLMNSTKTSGRAPAEVAFATPEMPSRDKRT 327
QY 484 LACLIQNFEPEDISVOWLHNEVOLPDARHSTTOPRKTKGS--GEFVSRLVETRAEMBOK 541
Db 328 LTLCLIQNFEPEDISVOWLHNEVOLPDARHSTTOPRKTKGS--GEFVSRLVETRAEMBOK 387
QY 542 DEFICRAVHAASPSQVQRAVSVPNG 568
Db 388 KQFTCOVTHALQKPRKLEKTSISLG 414

RESULT 10

QY 10 GCB_RAT STANDARD: PRT: 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: P50018; P50018.
DR HSSP: P01842; TEAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_Like; 1.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA: 36497 MW: 55F8B64D8D460A6 CRC64;

Query Match 26.6%; Score 813; DB 1; Length 333;
Best Local Similarity 63.6%; Pred. No. 5.2e-49;
Matches 145; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

QY 5 CDKHTCPPCAPPELLGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFKNVY 64
Db 106 CPTCTCHKCPVPELIGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFKNVY 165
QY 65 DGEVHNKTKRREBOYNSTYRVSVLYLVHONMNGKREKCKVNNKALPAPLEKTSISA 124
Db 166 NNEVHTAOTOPREBOYNSTYRVSVLYLVHONMNGKREKCKVNNKALPAPLEKTSISK 225

QY 125 KVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMESNGOPENNYKTPPYLD 184
Db 226 KGLVRRKPOVYVWGPPTEQLTQGVSLTCLTSGFLPNDIGVEMTSNGHTEKMYKKTPEYMD 285
QY 185 SVGSFELLSKITLVDSKRMQGNVSCSYMHALLNHHYQORLSLSLSPGK 232
Db 286 SDGSFEMYSKLINVERSDRSAPFVCSVYHGLHNVHKEKISRPPGK 333

RESULT 11

QY 11 GCB_MOUSE STANDARD: PRT: 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine Ig3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).

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CC EMBL: J00451; NOT_ANNOTATED_CDS.
CC DR PIR: B02156; G3MSC.
DR HSSP: P01857; 1RC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_Like; 1.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA: 36228 MW: F45827174182BAD6 CRC64;

Query Match 26.6%; Score 812.5; DB 1; Length 329;
Best Local Similarity 64.7%; Pred. No. 5.6e-49;
Matches 145; Conservative 35; Mismatches 41; Indels 3; Gaps 1;

QY 12 PP--CPAPELLGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFKNVYDGE 68
Db 106 PGGSSCPGNITIGSSVFLFPKPKDMLISLTLPKVTCTVVDVSHEDDPVHSMVFNKE 165
QY 69 VANNKTKRREBOYNSTYRVSVLYLVHONMNGKREKCKVNNKALPAPLEKTSISAKYOP 128
Db 166 VHTAMTOPREAOYNSTYRVSVLYLVHONMNGKREKCKVNNKALPAPLEKTSISKGRA 225
QY 129 REPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMESNGOPENNYKTPPYLDVSGS 188
Db 226 OTPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMESNGOPENNYKTPPYLDVSGS 285
QY 189 FFLYSKLTVDKSRMOGNNVSCSYMHALLNHHYQORLSLSLSPGK 232

RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.,
RT "Gene segments encoding transmembrane carboxyl termini of
RT Immunoglobulin gamma chains."
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE-8222190; PubMed-6283537;
RA Yamawaki-Katsoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT Immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.

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CC EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR PIR; B02159; GILSM.
DR HSSP; P01842; 7FAB.
DR MCD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302
FT TRANSMEM 340 357 POTENTIAL.
FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 25.68; Score 784.5; DB 1; Length 393;
Best Local Similarity 58.24; Pred. No. 5.9e-47;
Matches 135; Conservative 47; Mismatches 41; Indels 9; Gaps 3;

QY 2 PKSCDTHRCRP--CAPELLGSPVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVK 59
DB 99 PRCG-----CKPCICVPEV---SSVFIFPKPRDVLITLTPKVCVVVDISKDPEVQ 151
QY 60 FNNYVDGVEYHANKTKPREQYNSTYRVYSVLTVTLHOMNMGKREYKCKYVKNAALPAPIEK 119
DB 152 FSNFVDVDEYHTAQTPREQFNSTRYSVSELPIMHODWLNKREKCRVNSAAPAPIEK 211
QY 120 TISKAVQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 179
DB 212 TISKTRGRPRKAPQVYTLIPPKEQMKDKVSLTCLMIDTFPEFDITVEWQNGQPAENYKNT 271

QY 180 PPVLDVSGFPLYSKLTVDKSRWQGNVFGSVNHEALHNHYQQRSLSLSPG 231
DB 272 QPINTNGSYFVYSKLNWOKSNWEAGNTFTCSVLHEGILHNHTEKSLSHSPG 323

Search completed: July 15, 2003, 06:58:21
Job time : 18.7654 secs

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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:54:24 ; Search time 63.9554 Seconds
(without alignments)
1833.165 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDKHTPCPCAPAPPELL.....HEAAPSQTVQRAVSNVPGK 569

Scoring table: BLASTSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mmc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeophages: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	40.0	471	4	08TC77
2	1225	40.0	701	4	096P08
3	1097	35.8	473	4	08TC63
4	877.5	28.7	337	6	095M34
5	798.5	26.1	469	11	08R3V9
6	795.5	26.0	463	11	0991C4
7	791.5	25.9	437	11	09R1A4
8	782	25.6	473	11	09D814
9	772	25.2	468	11	0991J1
10	772	25.2	473	11	0991J2
11	752.5	24.6	473	11	091205
12	752.5	24.6	474	11	08R3H6
13	480.5	15.7	613	11	08VCX7
14	453.5	14.8	597	4	09B088
15	448.5	14.7	597	4	09B010
16	444	14.5	597	4	096B89

17	440.5	14.4	613	4	08WUK1
18	439.5	14.4	588	4	08WUX4
19	439.5	14.4	618	4	096AA6
20	438	14.3	614	4	096GA6
21	435	14.2	613	4	096EY0
22	413	13.5	375	4	09BS21
23	399	13.0	684	13	090544
24	356	11.6	416	4	09NPP6
25	354	11.6	496	4	096KX8
26	344.5	11.3	497	4	08WY24
27	344	11.2	494	4	096K68
28	340	11.1	384	4	09UP60
29	336.5	11.0	487	11	099KA4
30	335	10.9	482	11	091X92
31	334	10.9	496	4	096DK0
32	326.5	10.7	500	4	09BRV0
33	326	10.7	479	11	099M22
34	324.5	10.6	481	11	091W73
35	322.5	10.5	481	11	08VCV5
36	320	10.5	488	11	091WR1
37	319.5	10.4	484	11	099LA6
38	317	10.4	484	11	08VEA0
39	313.5	10.2	489	11	08VCX4
40	311	10.2	486	11	091Z07
41	309.5	10.1	481	11	091WT1
42	305	10.0	479	11	091WP5
43	302.5	9.9	480	11	091X61
44	301.5	9.9	426	11	09DCD9
45	235	7.7	573	4	08WU38

ALIGNMENTS

RESULT 1

ID	Query Match	Score	Length	DB ID	Description
08TC77	40.0%	1225	471	4	08TC77
AC	Best Local Similarity	97.0%	Pred. No. 1.6e-94		
DR	Matches	225	Conservative	3	Mismatches 4; Indels 0; Gaps 0;
DT	1	EPKSCDKHTPCPCAPAPPELLGSPVFLPPPKRDTLMSRTPEYCVVVDVSHDEPEVKF	60		
DR	240	EPKSCDKHTPCPCAPAPPELLGSPVFLPPPKRDTLMSRTPEYCVVVDVSHDEPEVKF	299		
QY	61	NMYVDGVVHNWKTFRREOYNSTFRVSVLTVLHQMNMNGKCYCKVSNKALPAPDIKT	120		
DB	300	NMYVDGVVHNWKTFRREOYNSTFRVSVLTVLHQMNMNGKCYCKVSNKALPAPDIKT	359		
QY	121	ISKAKVQRPQVYVTLPPSRDELTKNOVSLTCLVKGFPSPDIJAVEMESNGOPENNYKTP	180		
DB	360	ISKAKVQRPQVYVTLPPSRDELTKNOVSLTCLVKGFPSPDIJAVEMESNGOPENNYKTP	419		
QY	181	PYLDVSGFPLXSKITLVKSRWOCGNVSCSMHMLNNHQKSLSPK	232		

Db 420 PVLDSGSEFLYSLKLVYDKSRMOQGNFSCSVMHLEALHNHYTKSLSPCK 471

RESULT 2

096P08 ID 096P08 PRELIMINARY; PRT: 701 AA.
 AC 096P08;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Factor VII active site mutant immunocoujugate.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21477448; PubMed=11593034;
 RA Hu Z., Garen A.;
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
 cells for immunotherapy in mouse models of prostatic cancer.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
 DR EMBL; AF272774; AAKS8686.1; -
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF 2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; Ylkr_dep_GIA.
 DR Pfam: PF00008; EGF 2.
 DR Pfam: PF00594; g1a; 1.
 DR Pfam: PF00047; Iq; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR SMART; SM00181; EGF; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF 2; UNKNOWN_1.
 DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_DOM; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42CC992F CRC64;

Query Match 40.0%; Score 1225; DB 4; Length 701;
 Best local Similarity 97.0%; Pred. No. 2.8e-94;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCCKTHPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEVKF 60
 DB 470 EPKSCCKTHPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEVKF 529
 QY 61 NMVYDGEVHNATKREEDYNSTYRVSVLTVLHOMNMNGKEKCKVSKALPAPIEKT 120
 DB 530 NMVYDGEVHNATKREEDYNSTYRVSVLTVLHOMNMNGKEKCKVSKALPAPIEKT 569
 QY 121 ISRAKVGPREPQYVTLPPSHDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNKTTTP 180
 DB 590 ISRAKVGPREPQYVTLPPSHDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNKTTTP 649
 QY 181 PVLDSGSEFLYSLKLVYDKSRMOQGNFSCSVMHLEALHNHYTKSLSPCK 232
 DB 650 PVLDSGSEFLYSLKLVYDKSRMOQGNFSCSVMHLEALHNHYTKSLSPCK 701

RESULT 3

08TC63 ID 08TC63 PRELIMINARY; PRT: 473 AA.
 AC 08TC63;
 DT 01-JUN-2002 (Tremblrel. 21, Created)

DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 52.0 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025985; AAR25985.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 35.8%; Score 1097; DB 4; Length 473;
 Best local Similarity 90.5%; Pred. No. 9.3e-84;
 Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 11 CPCCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEKFMVYDGEVH 70
 DB 252 CPCCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEKFMVYDGEVH 311
 QY 71 NVKTKPREEQNSTYRVSVLTVLHOMNMNGKEKCKVSKALPAPIEKTISKAKVPRE 130
 DB 312 NAKTKPREEQNSTYRVSVLTVLHOMNMNGKEKCKVSKALPAPIEKTISKAKVPRE 371
 QY 131 PÖVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNKTTTPVLDGSGSF 190
 DB 372 PÖVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNKTTTPVLDGSGSF 431
 QY 191 LYSKLVYDKSRMOQGNFSCSVMHLEALHNHYTKSLSPCK 232
 DB 432 LYSKLVYDKSRMOQGNFSCSVMHLEALHNHYTKSLSPCK 473

RESULT 4

095M34 ID 095M34 PRELIMINARY; PRT: 337 AA.
 AC 095M34;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Immunoglobulin gamma 1 heavy chain constant region
 DE (Fragment).
 GN IGH1.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wagner B.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98383416; PubMed=9717671;
 RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
 Raibold W., Radbruch A.;
 RT "Organization of the equine immunoglobulin heavy chain constant region
 genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
 RL Immunobiology 199:105-119(1998).
 DR EMBL; AJ300675; CAC44624.1; -
 DR InterPro: IPR003006; Iq_MHC.
 DR Pfam: PF00047; Iq; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2;
 FT NON_TER 1
 SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 28.7%; Score 877.5; DB 6; Length 337;
 Best local Similarity 67.7%; Pred. No. 1.6e-65;
 Matches 157; Conservative 36; Mismatches 36; Indels 3; Gaps 2;

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QY 3 KSCDKHTCPCCPPELLGSPVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFM
DB 107 KVCQMS-KCPKCAPPELLGSPVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFM 165
QY 63 YVDGVEVHNKTKPREEOYNSTYRVSVLYLHONMNGKEYCKVSKALPAPIETIS 122
DB 166 YMDSEVETATTPREKEDQFNSTRVSVLYLHODMLSGKEFKCKVNOALPAPIETIT 225
QY 123 KAKVQPREOYVTLPPSRDELTKNOVSLTCLVKGFYSDDIAVEHESNQ--ENNYKTP 180
DB 226 KTKGRSEPOVYVLAHPDELISKVSVTCLVKDFPEPELNIEMQSNQPLELTKRYSTQ 285
QY 181 PVLDSVGSFFLYSKLTVDKSRMOOGNVSVMHEALHNHYOQSLSLSPGK 232
DB 286 AQDSDSGSYFLYSKLSYDRNMQOGTFTGCVMEALHNHYOQSLSLSPGK 337

RESULT 5
Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC O8R3V9
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024405; AA024405.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 26.1%; Score 798.5; DB 11; Length 469;
Best Local Similarity 59.2%; Pred. No. 1.2e-58;
Matches 138; Conservative 45; Mismatches 41; Indels 9; Gaps 3;

QY 2 PKSCDKHTCP--CPAPELLGSPVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVK 59
DB 244 PROCG---CKPCICTVPEV---SSVFIFPPKPKDVLITLTPKVTGVVDVSHEDPEVQ 296
QY 60 FNNVYDGEVHNKTKPREEOYNSTYRVSVLYLHONMNGKEYCKVSKALPAPIEK 119
DB 297 FSWFVDVDEVHTAOTPREEOFNSTFRVSELPIMHODMLNGKEFKCVNSAAPAPIEK 356
QY 120 TISAKVQPREOYVTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEHESNGOPENNYKT 179
DB 357 TISTKGRKAPQVYITTPREKQAKDKVSLTCLTDFPEDIYEWQMNQAPENYKNT 416
QY 180 PVLDSVGSFFLYSKLTVDKSRMOOGNVSVMHEALHNHYOQSLSLSPGK 232
DB 417 QPIMDTGSGSYFLYSKLVNOKSNMEAGNFTCSVLHGLHNHTEKSLSHSGK 469

RESULT 6
Q991C4 PRELIMINARY; PRT; 463 AA.
AC O991C4
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AA03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_c1.
DR InterPro; IPR003606; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; Ig; 2.
DR SMART; SM00406; Ig; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; 5AA674C6B6C30783 CRC64;

Query Match 26.0%; Score 795.5; DB 11; Length 463;
Best Local Similarity 58.8%; Pred. No. 2e-58;
Matches 137; Conservative 46; Mismatches 41; Indels 9; Gaps 3;

QY 2 PKSCDKHTCP--CPAPELLGSPVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVK 59
DB 238 PROCG---CKPCICTVPEV---SSVFIFPPKPKDVLITLTPKVTGVVDVSHEDPEVQ 290
QY 60 FNNVYDGEVHNKTKPREEOYNSTYRVSVLYLHONMNGKEYCKVSKALPAPIEK 119
DB 291 FSWFVDVDEVHTAOTPREEOFNSTFRVSELPIMHODMLNGKEFKCVNSAAPAPIEK 350
QY 120 TISAKVQPREOYVTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEHESNGOPENNYKT 179
DB 351 TISTKGRKAPQVYITTPREKQAKDKVSLTCLTDFPEDIYEWQMNQAPENYKNT 410
QY 180 PVLDSVGSFFLYSKLTVDKSRMOOGNVSVMHEALHNHYOQSLSLSPGK 232
DB 411 QPIMDTGSGSYFLYSKLVNOKSNMEAGNFTCSVLHGLHNHTEKSLSHSGK 463

RESULT 7
Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; Ig; 1.
DR SMART; SM00410; Ig_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

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	Query Match	25_98:	Score	791.5:	DB	11:	Length	437:
	Best Local Similarity	58.4%:	Pred.	No.	4.1e-58:			
	Matches	136:	Conservative	47:	Mismatches	44:	Indels	9:
							Gaps	3
Oy	2	PKSCDKTHTCP--CPAPDLLGGPSVLEFPKPKDLMISRTPEYTCVVVDVSHEDPEVK	59					
Db	212	PRDCG---CPCICITVEEV---SSVFIFPKPKDVLITLTPKLCVVVIDISKDDPEVQ	264					
Oy	60	FNMVVDGEVAVNVTKKPREEOYNSTVRVSVTTLTHOMMNGKEVCKCVSNALPAPIEK	119					
Db	265	FSWIVDYDEVTTAQTQPRNEOPNSTFRSVSELPITHOOLNKCEKCRNSAAFPAPIEK	324					
Oy	120	TISKAQVQRPQQYTTPRSDELTKNOVSLTCLVKGEPSPSDIAEWESNGPENNRYTT	179					
Db	325	TISTTKGRPKAPQVYTTIPRKEOMAKDKVSLTGMTDFPEDDITVEWMQNGPAENRYKT	384					
Oy	180	PPVLDSGSPFLYSKLTVDRKSMMQGNFSSCSVMHEALAHNHQOKSLSPK	232					
Db	385	QPIMDTDSIYIVSKLVAKYKNMEGNFTFCVLTGEGJLNHNHTEKNLSLSPK	437					

RESULT 8			
09DBL4			
ID	09DBL4	PRELIMINARY;	PRT: 473 AA.
AC	09DBL4;		
DT	01-JUN-2001 (TRENBLREL. 17, Created)		
DT	01-JUN-2001 (TRENBLREL. 17, Last sequence update)		
DT	01-DEC-2001 (TRENBLREL. 19, Last annotation update)		
DE	1810060009RIK protein.		
GN	IGH-1 OR 1810060009RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Adachi J., Fukuda S.,		
RA	Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Iwawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,		
RA	Sato T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,		
RA	Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Giusticich S., Hill D., Hofmann M., Hume D.A., Kamlaya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,		
RA	Wysshaw-Bouris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
DR	HSSP, P01842; 7FAB.		
DR	EMBL, AK007918, BAB25349.1; -.		
DR	HSSP, P01842; 7FAB.		
DR	MGD, MGI:96443; Igh-1.		
DR	InterPro: IPR003599; Ig.		
DR	InterPro: IPR003597; Ig-cl.		
DR	InterPro: IPR003600; Ig-llike.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_v.		
DR	Pfam: PF00047; Ig_4.		
DR	SMART, SM00409; Ig_2.		
DR	SMART, SM00407; Igcl_3.		
DR	SMART, SM00406; IGV_1.		
DR	SMART, SM00410; Ig_llike_1.		
DR	PROSITE, PS00290; IG_MHC; UNKNOWN_1.		

[illegible]

RESULT 9					
ID	Q99LJ31	PRELIMINARY;	PRT:	468 AA.	
AC	Q99LJ31;				
DT	01-JUN-2001 (TREMBLE)	17,	(Created)		
DT	01-JUN-2001 (TREMBLE)	17,	Last sequence update)		
DT	01-JUN-2002 (TREMBLE)	21,	Last annotation update)		
DE	Similar to RIKEN cDNA 1810060009 gene.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Straussberg R.;				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; BC003878; AAH03878.1;		-		
DR	HSSP; P01842; 7FAB.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR003597; Ig_c1.				
DR	InterPro; IPR003600; Ig_like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_3.				
DR	SMART; SM00409; Ig; 2.				
DR	SMART; SM00407; Igcl; 3.				
DR	SMART; SM00406; IgV; 1.				
DR	SMART; SM00410; IG_Like; 1.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.				
SO	SEQUENCE	468 AA;	51661 MW;	96352328B332ADB	CRC64;
Query Match					
Best local similarity 25.2%; Score 772; DB 11; Length 468;					
Matches 141; Conservative 31; Mismatches 50; Indels 2; Gaps 1;					
QY	11 CPE--CPAPELLGGPSVFLEPPPKDKDTLMISRTEPVTCVVVDVSHEDEPVKFNMYDVGVE	68			
DV					
QY	245 CPCKPCAPAPNLGGSPVFIEPPRKIDVLIMTSLSPMVCVVVDSEDDPDVQISMFFVNWE	304			
DV					
QY	69 VHNWKTTPREDOYNSTRVYSVLTVLHQNMNGKEFKCYKSNNKALPAPIETTKISKAYQP	128			
DV	: : : : : : : : : : : : : : : : : : :				
DV	305 ULTAQOTDTHREDNSTLRVVSALPIQHODMWSGKEFKCYKNKKALPAPIETTKISKPGSV	364			
QY	129 REPQVYTLPPSRDELTKNOYSLFTGLVGFGYPDSIDAVEMESNGOEPNNKTPVPYLDVSGS	188			
DV					
DV	365 RAQGVYTLPPPEELMTKKQTLLTCMVTDMPEDILYEKTNNGKTELNTKNTPELVDSGS	424			
QY	189 FFLYSKLTVDKSRMQOGNVFSCSYMHDLAHNYOQRSLSLSPGK	232			
DV					
DV	425 YFMKSKLRYEKKNNVERNSYSCSYVHGHLHHHTTKSFSPGK	468			

AC Q8VXC7; 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
OS Hypothetical 67.9 kDa protein.
OC Mus musculus (Mouse).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SALIVARY GLAND;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC018315; AAH18315.1; -
DR InterPro: IPR003599; IG_c1.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_5.
DR SMART: SM00409; IG_2.
DR SMART: SM00407; IGc1; 4.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
DR Hypothetical protein.
KW SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
SQ

Query Match 15.7%; Score 480.5; DB 11; Length 613;
Best Local Similarity 28.5%; Pred. No. 9.5e-32;
Matches 133; Conservative 77; Mismatches 205; Indels 51; Gaps 15;

QY 120 TISKAKYOPREPOVYTLPPSRDELTKNOVSLTCLVGFYPSDIAVEMESGQENNYKT 178
DB 132 TVVYSSSSQSPFNPFLVSCSPISDKNLVAMGLADELPSTISFTWNY---NNTEV 187
QY 179 ----TPVLDVSGSFLLYSKLTVDKSRMOG--VFSCSYMHDLNHYOQRLSLTS-- 229
DB 188 IGGIRTEPLRLTGKYLATSOVLLSPKSLIEGSDVLYCKI-----HYGKRRLDHPV 240
QY 230 -PGKVEGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 287
DB 241 IPAYAE-----MNPNNVNVPPRDGSGGAPRKSKLICENTVNTPPKPI 284
QY 288 ITWLEDQAVDVLSTASTOEGELASTQ-----SELTLSOKHMLSDRTYCOVYOGHT 342
DB 285 VSNLKDOKLIVSGSTTTPVLTENKSGTPQYKIVSTLTISEIDMLNLTAVTTCRDHAGLT 344
QY 343 F-EDSTKCKADSNRGSAYLSRSPDLFTRKSPITTCVLVDLAPSKGVNLWRSRAG 401
DB 345 FLNVSSTCAASPTDILFTFTIPPSFADIFLSKANLTCVSNLATEY-TLNISMASQSG 403
QY 402 KPNVHSTRKEKQRNGLTYSSTLPVGRDMIEBETQCVRTHHPLRALMRSTTKSGP 461
DB 404 EPLETKIKIMESHDPNGFTSSAKGVASVCEEDMNNKEVECTVTHDLPSPKKFISKNEV 463
QY 462 RAPEYVAFATP--EMPGSRDKRTIACLIQNFMPEDISVOMLHNEVOLPDARHSTTOPRK 519
DB 464 HKRPANVYLLPAREQNLRESATVYCLVKGFSADISVOMLORGQLLPCKYTSAPMP 523
QY 520 TKGS-GF-FVFSKLEVTTRAEMEQKDEFICRAVHAASPSQTVORAV 563
DB 524 EPQAPGFFYTHSILTVTEEMNSGETYTCVAGHEAL-PHLVTERTV 568

RESULT 14

ID 09BOB8 PRELIMINARY; PRT; 597 AA.

AC 09BOB8; 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Unknown (protein for MGC:1905) (protein for MGC:1228).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MUSCLE;
RA Strauberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPH;
RA Strauberg R.;
RL Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC001872; AAH01872.1; -
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003599; IG_c1.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003600; IG_c1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_5.
DR SMART: SM00409; IG_2.
DR SMART: SM00407; IGc1; 4.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
DR SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
SQ

Query Match 14.8%; Score 453.5; DB 4; Length 597;
Best Local Similarity 24.6%; Pred. No. 1.7e-29;
Matches 143; Conservative 97; Mismatches 266; Indels 75; Gaps 21;

QY 31 KPKDTLMSIRTEPYTCVVDVS-----HEDPEKFNMYVD-----GVEVHNYKTKPR 77
DB 32 KPSETL-----SLTCGVYGGSGFYXWMTROPPGAGLEIGGINSGITNYPISLKR 85
QY 78 EEOYNSTYRVVSVTLVHLQNMNCKEYK-KVSKKALPAPIEK-----TISKAV 126
DB 86 VTSVDTSKKQLSLKLSVNAADPAVYVCARVITRASPGTDGGRVGMWGGGTIVVSSG 145
QY 127 QPREPOVYTL-----PESRDELTKNOVSLTCLVGFYPSDIAVEMESGQENNYKTTP 180
DB 146 SASKPTLFPVLYSCNSNS-----DTSVAVGLADELPDSTTSWKTKNNSDISSTGFP 201
QY 181 PVLDVSGSFLLYSKLTVDKSRMOG--VFSCSYMHDLNHYOQRLSLSPKVEGGGG 238
DB 202 SVLNG-GKYAATSGVLLPSKDVMOGTDEHVCKVQHP--NGNKKNVPL-PVIAE---- 252
QY 239 SGGGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 298
DB 253 -----LPPKVSFVPPRDGSGGAPRKSKLICENTVNTPPKPI 300
QY 299 VDLSTASTOEGELA-----STOSELTLISOKHMLSDRTYCOVYOGHT-EDSTKCAD 352
DB 301 SGVTTDVOVAEAKESGTTTKYVSTLTIKSDMLSGMFLPCRDHRLTQOQNSSMCPV 360
QY 353 SNRGSAYLSRSPDLFTRKSPITTCVLVDLAPSKGVNLWRSRAGRPVNHSTREE 412
DB 361 DQDAIRVFAIPSPFASIFLTKSTKLCLVTLDT-TVDSTVTSMTQNGAVVTHNISE 419
QY 413 KQNGTILTVSTLPVGRDMIEBETQCVRTHHPLRALMRSTTKSGPRA-APEYVAF- 470
DB 420 SHPNATFSAVGEASIEDDWSNGERTCTVTHDLPSPKQTLSPKGVALLHPRDYLPL 479
QY 471 ATPEMGSRDKRTIACLIQNFMPEDISVOMLHNEVOLPDARHSTTOPR-KTKGSG-FEVE 528
DB 480 PAREQNLRESATITCLVTSFSPADYVOMOGQPSPEKTYTSADMPPOAPGRIFAH 539
QY 529 SRLVETRAEMEQKDEFICRAVHAASPSQTVORAVSNPCK 569
DB 540 SILTVSEEWNTGETYTCVAGHEAL-PNRYTERTVKSTCK 579

RESULT 15
09BUI0 PRELIMINARY; PRT; 597 AA.
AC 09BUI0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Hypothetical 65.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1;
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003597; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 14.7%; Score 448.5; DB 4; Length 597;

Best Local Similarity 24.6%; Pred. No. 4.5e-29;
Matches 143; Conservative 96; Mismatches 267; Indels 75; Gaps 21;

QY 31 KPKDTLMISRPETVCVVVDS-----HEDPEVKFNMYVD---GVEVHNKTKRPR 77
DB 32 KPSETL-----SLTCGVYGGSGFYWSWIRPPGKLEWIGEHNSGSTNPNLSKSR 85
QY 78 EEOYNSTYRVVSVTLVHOMMNGKEYK-KVSNKALPAPIE-----TISKAVY 126
DB 86 VTISVDTSKKOLSLKLSVNAADAVYYCARVITRASPGTDGRGMVWGQGTIVTVSSG 145
QY 127 QPREPQVYTL-----PPSRDELTKNQSLSLCLVKGFTPSDIAVEWE-SNGQENNNYKTP 180
DB 146 SASAPTLFPLVSCNSPSS---DTSSVAVGCLAODFLPDSITFSMKYKNNSDISSTRGFP 201
QY 181 PVLDSVGSFLLSKLTVDKSNMOG--NVFSCSVMEALHNHYOQRSLSLSPGKVEGGCG 238
DB 202 SVLRG-GKIATTSOVLPLPSKDVMOGTDEHYVVKQHP--NGNKEKNVPL-PVIAE---- 252
QY 239 SGGGSGSGGSGFTPTVKILQSSCGGSHPEPTIQLCLVSGYPTGTTINITWLEDQVMD 298
DB 253 -----LPPKVSVPFPRDGFQGNPKRSKLLIQAGTSPQIQVSWLREGQVYG 300
QY 299 VDLSTASTOGEGLA-----STOSELTLQKHWLSDRTYTCQVYQGHF-EDSTKRCAD 352
DB 301 SGVTTDOVOAEAKESGPTTYKVTSTLIKESDWLSOSMFTCRVDHRCGLTFEQNASSMCVP 360
QY 353 SNPRGVSAYLSRPPFLFIRKSPITICLVVDLAPSKGTVLTWSRASGKPVNHNSTRKEE 412
DB 361 DQDTAIRFALPFPFASIFLTKSLTKLCLVYDLT-TYDSVTISWTRONGEAVKTHNISE 419
QY 413 KORNGTLVSTLPEVGRDWIEGFTYQCRVTHPHLPALMRSTTKTSGPRA-APEVYAF- 470
DB 420 SHPNATFSAVGEAISEDMDNMGSERFCTVHTHDLPSPLKQTIISRPKGVALLHRDVIILP 479
QY 471 ATPPEPSRDKRTIACLIONMPEDISYQWILHNEVQLPDARHSTTOR-KTKSGG-FFVF 528
DB 480 PAROLNLRSATITTCIVTGFSPADVFQWMOGQPLSPKRYVTISAPWPEQADPGRYFAH 539

OY 529 SRLVTPRAEWQKDEFICRAVHAASPSQTVORAVSNPGR 569
DB 540 SILTVSEEWNTGETTYCVVAHRL-PNRVTEKTVDKSTOK 579

Search completed: July 15, 2003, 07:01:49
Job time : 64.9554 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:46:49 ; Search time 67.0009 Seconds
(without alignments)
1131.621 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDTHRCPCAPPELL.....HEAAPSQTVQRAVSVPNGK 569

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A.Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1983.DAT:*
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- 20: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1999.DAT:*
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- 22: /SIDS2/gcgdata/geneseq/genesep-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/genesep-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1766	57.7	428	23	AAU80283
2	1766	57.7	428	23	AAU50940
3	1766	57.7	428	23	AAU47863
4	1760	57.5	493	5	AAU40065
5	1755	57.4	441	5	AAU80287
6	1723	56.3	428	14	AAU42950
7	1707	55.8	323	23	AAU80284
8	1707	55.8	323	23	AAU80285
9	1707	55.8	323	23	AAU80286
10	1707	55.8	324	16	AAU83559

11	1707	55.8	325	16	AAU75225
12	1707	55.8	325	16	AAU77241
13	1707	55.8	331	21	AAU03642
14	1707	55.8	367	9	AAU80291
15	1701	55.6	325	21	AAU79994
16	1696	55.4	336	23	AAU80288
17	1685	54.8	325	16	AAU83582
18	1677	54.8	315	16	AAU85582
19	1671	54.6	330	23	AAU80289
20	1273.5	41.6	711	20	AAU85692
21	1267	41.4	689	21	AAU86780
22	1251.5	40.9	689	21	AAU96779
23	1247	40.8	277	21	AAU16967
24	1247	40.8	277	23	AAU73418
25	1243	40.6	268	21	AAU16959
26	1243	40.6	268	23	AAU73412
27	1243	40.6	268	21	AAU96531
28	1242.5	40.6	448	21	AAU28694
29	1241	40.6	426	21	AAU28695
30	1234.5	40.3	731	22	AAU52156
31	1234.5	40.3	741	22	AAU52159
32	1232.5	40.3	423	21	AAU28693
33	1232	40.3	660	20	AAU13463
34	1232	40.3	660	21	AAU28523
35	1232	40.3	660	22	AAU70132
36	1232	40.3	660	22	AAU31694
37	1229	40.2	379	19	AAU83962
38	1229	40.2	379	19	AAU49073
39	1226	40.1	253	21	AAU16964
40	1226	40.1	253	23	AAU73415
41	1226	40.1	652	19	AAU48650
42	1225	40.0	232	18	AAU26232
43	1225	40.0	232	21	AAU28690
44	1225	40.0	232	22	AAU72915
45	1225	40.0	232	22	AAU80897

ALIGNMENTS

RESULT 1	AAU80283	AAU80283 standard; Protein; 428 AA.
ID	AAU80283;	
AC	AAU80283;	
XX		
DT	30-JUL-2002	(first entry)
DE	Human Ige heavy chain C1-C2-C3-C4 domains.	
DE	Ige; allergy; human; antiallergic; immunosuppressive; antianaphylactic;	
KW	antiallergic; dermatological; antinflammatory; immunoglobulin E; Ige;	
KW	vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;	
KW	heavy chain C domain.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Domain	11..116 "Ige heavy chain C1 domain"
FT	Domain	113..208 "Ige heavy chain C2 domain"
FT	Domain	205..219 "Ige heavy chain C3 domain"
FT	Region	/note="Epitope including C2C3 linker"
FT	Region	209..216 "Linker domain between C2 and C3 region"
FT	Domain	217..316 "Ige heavy chain C3 domain"
FT	Region	244..251 "Epitope in BC loop"
FT	Region	244..251 "Epitope in BC loop"
FT	Region	/note="Epitope in BC loop"
FT	Region	272..280

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FT FT /note="Epitope in DE loop"
FT Region 301..311
FT /note="Epitope in FG loop"
FT Region 315..323
FT /note="Epitope including C3C4 linker"
FT Region 317..320
FT /note="Linker between domains C3 and C4"
FT Domain 321..422
FT /note="Ige heavy chain C4 domain"
PN WO200220038-A2.
PD 14-MAR-2002.
XX
XX
XX 06-SEP-2001; 2001WO-DK00579.
XX
XX 06-SEP-2000; 2000DK-0001326.
XX PR 15-SEP-2000; 2000US-232831P.
XX
XX (PHAR-) PHARMEXA AS.
XX
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX WPI: 2002-383033/41.
XX
XX Inducing immune response against autologous immunoglobulin E in an
XX animal, by effecting simultaneous presentation of cytotoxic T
XX lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
XX
XX Examples; Page 101-103; 151pp; English.
XX
XX This invention relates to a novel method for inducing an immune response
XX against autologous immunoglobulin E (Ige) in an animal. The method
XX comprises effecting simultaneous presentation of cytotoxic T lymphocyte
XX (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
XX epitope (TH epitope) which is foreign to the animal, by antigen
XX presenting cells (APCs) of the animal's immune system. The epitopes
XX of the invention may be used as a vaccine against allergic diseases. The
XX method of the invention is useful for inducing an immune response
XX against autologous Ige in an animal, which is useful for downregulating
XX autologous Ige in the animal. This method is useful in the prevention
XX and treatment of allergic diseases such as anaphylaxis, allergic
XX rhinitis, asthma and atopic dermatitis. The present sequence represents
XX the human Ige heavy chain C1-C2-C3-C4 domains used to create the
XX epitopes of the invention.
XX
XX Sequence 428 AA:
SQ
Query Match 57.7%; Score 1766; DB 23; Length 428;
Best Local Similarity 78.0%; Pred. No. 9.5e-115;
Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;
OY 129 REPQVYLPSSRDELTKNOVSLT--CLVKGFPSDIAVWESNGOPENNYKTP-PVLDS 185
DB 4 QSPSVFPLTRCKKIPSNATSVTLGLATAGFPEPVMTWDT-GSLNQTWTLPATLTLL 62
OY 186 VGSFPLYSKLLVDSRNQGVNFCGVNHEALNHHY-QQRLSLSPKGVBEGGSGGGGS 244
DB 63 SGHATYISLTV-SGAWAK-OMFTCRVAHPSSTIDWDNKFFVC----- 105
OY 245 GGGSGFTPTPYKIIQSSCDGGHPPPTIQLCLVSGYTPGTINTTWLEDGVMDLSTA 304
DB 106 --SNDFFPPYKIIQSSCDGGHPPPTIQLCLVSGYTPGTINTTWLEDGVMDLSTA 163
OY 305 STTQEGELASTQSELTLISQKHWLSDRYTCQVTVQGHTEFEDSTKCADSNRGVSAVLSR 364
DB 164 STTQEGELASTQSELTLISQKHWLSDRYTCQVTVQGHTEFEDSTKCADSNRGVSAVLSR 223
OY 365 PSPPDLIRKSPPTTCLVNDLAPSKGVNLTWMSASGKPVNHSRKEEKQNGTLTYTST 424
DB 224 PSPPDLIRKSPPTTCLVNDLAPSKGVNLTWMSASGKPVNHSRKEEKQNGTLTYTST 283

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OY 425 LPVGRDMEIGETTQCRVTHPLPALMRSTTKTSGPPRADEYVAFATPEWPGSRDKRTL 484
DB 284 LPVGRDMEIGETTQCRVTHPLPALMRSTTKTSGPPRADEYVAFATPEWPGSRDKRTL 343
OY 485 ACLIONFPEPDISVQMLNEVQLPDARHSTTOPRTKSGGFVSRLEVTAEWPKDEF 544
DB 344 ACLIONFPEPDISVQMLNEVQLPDARHSTTOPRTKSGGFVSRLEVTAEWPKDEF 403
OY 545 ICRAYHEAASPSQTVQRAVSNPGR 569
DB 404 ICRAYHEAASPSQTVQRAVSNPGR 428

RESULT 2
AAM50940
ID AAM50940 standard; Protein; 428 AA.
XX
XX AAM50940;
AC
XX
DT 15-MAY-2002 (first entry)
DE Human Ige epsilon chain constant region.
XX
XX Ige: immunoglobulin E; antibody; human; allergy; asthma; eczema;
XX urticaria; anaphylactic shock; allergic rhinitis; conjunctivitis;
XX anti-anaphylactic; immunosuppressive; antiallergic; antisthmatic;
XX antinflammatory; dermatological; vasotropic; ophthalmological;
XX vaccine; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 1..110
FT /label= CH1
FT 313..428
FT Domain /label= CH4
XX
XX WO200209751-A2.
XX
XX 07-FEB-2002.
XX
XX 23-JUL-2001; 2001WO-1B01353.
XX
XX 28-JUL-2000; 2000US-221841P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX (BACH/) BACHMANN M F.
XX (RENN/) RENNER W A.
XX
XX Bachmann MF, Renner WA;
PI WPI: 2002-227076/28.
XX
XX Composition for treating immunoglobulin (Ig) E-mediated disorder such
XX as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises
XX a polypeptide that includes CH1 and/or CH4 domains of Ige molecule
XX coupled to a carrier.
XX
XX Claim 41; Page 9; 71pp; English.
XX
XX The present sequence is that of the human Ige epsilon chain
XX constant region. The invention is based on the discovery that a
XX polypeptide that includes the CH1 (i.e. constant domain 1 in the
XX heavy chain) and/or CH4 domain(s) of an Ige molecule, coupled to a
XX carrier, can be used to induce in a mammal the production of
XX antibodies that specifically bind to Ige of the mammal.
XX Compositions are provided for inducing self-specific anti-Ige
XX antibodies. These contain carriers foreign to the immunised mammal
XX coupled to polypeptides containing fragments of the Ige molecule,
XX especially fragments including the constant CH1 and/or CH4 domain,
XX but not the CH3 domain. CH1 polypeptides have at least 95% identity
XX to amino acids 1-110, 105, 5-105 or 5-95 of the present sequence,
XX while CH4 polypeptides have at least 95% identity to amino acids

```


RESULT 4

ID AAP40065 standard; Protein; 493 AA.

AAP40065;

12-FEB-1992 (first entry)

Sequence of human immunoglobulin E H-chain.

Antibody; allergy suppressor; immunological.

Homo sapiens.

EPI02634-A.

14-MAR-1984.

03-SEP-1983; 83EP-0108699.

07-SEP-1982; 82JP-0156285.

(TAKE) TAKEDA CHEMICAL IND KK.

Kikuchi M, Kurokawa T, Onda H;

WPI: 1984-070437/12.

N-PSDB; AAN40062.

Polypeptide having activity of human immunoglobulin E - prep.

from host transformed with recombinant DNA

Disclosure: Fig 2; 61pp: English.

DNA encoding IGE H-chain and frags. is claimed (AAN40062).

Transformant contg. the DNA is also new, esp. Escherichia coli IFO-14284, -5 and -6. The transformant may be grown to produce a

polypeptide of immunological or biological activity equivalent to that of the human IGE H chain. AAN40062 or frags. is pref. linked at a

site downstream from a promoter, e.g. rec A promoter (see AAN40064).

Sequence 493 AA;

Query Match 57.5%; Score 1760; DB 5; Length 493;

Best Local Similarity 77.0%; Pred. No. 3e-114; Mismatches 66; Indels 24; Gaps 7;

Matches 349; Conservative 14; Mismatches 66; Indels 24; Gaps 7;

120 TISRAKYQPREPOVYTLPPSRDELTKNOVSLT--CLVKGFPSPDIAMWESNGOPENNYK 177

62 TVSSASTQ--SPSYEPILRCKKNIPSNATSVTLGCLATGYPPEPVMTWDT-GSLNGTMM 118

178 TTP-PVLDVSGSFPLYKLYDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPKVEGG 236

119 TLPATTTLLSGHYATISLTV--SGAMAK-QIFTCRAVATTPSSTWVDNXTF----- 167

237 GSGSGGGGGGSGTTPPVKILQSSCDGGHFPPTIOLCLVSGYTPGTITITLWEDGOV 296

168 -----SVCGRDTPPTVKILQSSCDGGHFPPTIOLCLVSGYTPGTITITLWEDGOV 220

297 MDVLDLASTQEGELASTOSELTLISQKHWLSDRTYTCOVYQGHTEFEDSTKKCADSNPR 356

221 MDVLDLASTQEGELASTOSELTLISQKHWLSDRTYTCOVYQGHTEFEDSTKKCADSNPR 280

357 GVSAYLSRPFDFLIRKSPITITLVVDLAPSKGTVALTWSRASGKPVNSTRKEKORN 416

281 GVSAYLSRPFDFLIRKSPITITLVVDLAPSKGTVALTWSRASGKPVNSTRKEKORN 340

417 GTLVFTSLPVGTRDWTLEGEEYQCRVTHPHLPRALMSTPTSGPRAPAYATATPEMP 476

341 GTLVFTSLPVGTRDWTLEGEEYQCRVTHPHLPRALMSTPTSGPRAPAYATATPEMP 400

QY 477 GSRDKRTIACLIQNPEDISYQWLHNEVQLPDANHSTQPRKTKGSGFPVFSRLVTRA 536

DB 401 GSRDKRTIACLIQNPEDISYQWLHNEVQLPDANHSTQPRKTKGSGFPVFSRLVTRA 460

QY 537 EWEOKDEFICRAVHEAASPSOTVORAVSVNGK 569

DB 461 EWEOKDEFICRAVHEAASPSOTVORAVSVNGK 493

RESULT 5

ID AAB0287 standard; Protein; 441 AA.

AAB0287;

30-JUL-2002 (first entry)

Human IGE heavy chain C1-C2-C3-C4 domains with MIGIS fragment.

IGE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;

antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IGE;

vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;

heavy chain C domain; MIGIS.

Homo sapiens.

Synthetic.

Key

Location/Qualifiers

11..106

/note="IGE heavy chain C1 domain"

113..208

/label="IGE heavy chain C2 domain"

205..219

/note="Epitope including C2C3 linker"

209..216

/note="Linker domain between C2 and C3 region"

217..317

/note="IGE heavy chain C3 domain"

244..251

/note="Epitope in BC loop"

244..251

/note="Epitope in BC loop"

272..280

/note="Epitope in DE loop"

301..311

/note="Epitope in FG loop"

315..323

/note="Epitope including C3C4 linker"

318..320

/note="Linker between domains C3 and C4"

RESULT 5

ID AAB0287 standard; Protein; 441 AA.

AAB0287;

30-JUL-2002 (first entry)

Human IGE heavy chain C1-C2-C3-C4 domains with MIGIS fragment.

IGE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;

antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IGE;

vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;

heavy chain C domain; MIGIS.

Homo sapiens.

Synthetic.

Key

Location/Qualifiers

11..106

/note="IGE heavy chain C1 domain"

113..208

/label="IGE heavy chain C2 domain"

205..219

/note="Epitope including C2C3 linker"

209..216

/note="Linker domain between C2 and C3 region"

217..317

/note="IGE heavy chain C3 domain"

244..251

/note="Epitope in BC loop"

244..251

/note="Epitope in BC loop"

272..280

/note="Epitope in DE loop"

301..311

/note="Epitope in FG loop"

315..323

/note="Epitope including C3C4 linker"

318..320

/note="Linker between domains C3 and C4"

WPI: 2002-383033/41.

Klysner S, Von Hoegen P, Voldborg B, Gautam A;

06-SEP-2000; 2000DK-0001326.

15-SEP-2000; 2000US-232831P.

(PHAR-) PHARMA AS.

Inducing immune response against autologous immunoglobulin E in an

animal, by effecting simultaneous presentation of cytotoxic T

lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin

Examples; Page 116-117; 151pp; English.

This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C1-C2-C3-C4 domains fused to the M1G1S fragment used to create the epitopes of the invention.

Sequence 441 AA;

Query Match 57.4%; Score 1755; DB 23; Length 441;

Best Local Similarity 77.9%; Pred. No. 5,7e-114; Indels 24; Gaps 7;

Matches 345; Conservative 17; Mismatches 57; Indels 24; Gaps 7;

```

OY 129 REPQYVTLPPSRDELTKNOVSLT--CLYKGFPSDIAEWESNGCPENNYKTP-PVLD 185
DB 4 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMTWDT-GSLNGTMTLPTATLT 62
OY 186 VGSFELYKLYDKSRMOQGNFSCSVNHEALHNHY--OORSLISPGKVEGGSGGSGS 244
DB 63 SGHYATISILTY-SCAMAK-QMFTCRVAHPSSTWVNKTFEVC----- 105
OY 245 GGGSEFTPTPKYKILQSSCDGGGHPPTIOLCLVSGYTPGTINITWLEDGQVMDVLS 304
DB 106 ---SRFTPTPKYKILQSSCDGGGHPPTIOLCLVSGYTPGTINITWLEDGQVMDVLS 163
OY 305 STTQEGELASTOSELTLSQKHWLSDRTYCOVYTGHTFEDSTKKCADSNPRGVSAYLS 364
DB 164 STTQEGELASTOSELTLSQKHWLSDRTYCOVYTGHTFEDSTKKCADSNPRGVSAYLS 223
OY 365 PSFPLFTRKSPITITCLVVDLAPSKGTYNLTWSRAGKPVNHSRKEKORNGTLTVST 424
DB 224 PSFPLFTRKSPITITCLVVDLAPSKGTYNLTWSRAGKPVNHSRKEKORNGTLTVST 283
OY 425 LPVGRDMEIEGETYQCRVTHPHLPALMNSTKTSKGPRAAPEVYAFATPEWPGSRDKRTL 484
DB 284 LPVGRDMEIEGETYQCRVTHPHLPALMNSTKTSKGPRAAPEVYAFATPEWPGSRDKRTL 343
OY 485 ACLIONFMPEDISVQMLHNEVOLPDARHSTQPRKTKSGGFVFSRLEVTTRAWEQKDEF 544
DB 344 ACLIONFMPEDISVQMLHNEVOLPDARHSTQPRKTKSGGFVFSRLEVTTRAWEQKDEF 403
OY 545 ICRAYVHEAASPSQTYQRAVSNP 567
DB 404 ICRAYVHEAASPSQTYQRAVSNP 426

```

RESULT 6

AAR42950.

ID AAR42950 standard; protein; 428 AA.

XX AAR42950;

XX 12-MAY-1994 (first entry)

DE Human IgE heavy chain constant region (residues 120-547).

XX Immunoglobulin E; IgE; epsilon heavy chain; IgE receptor binding;

KW FcR region; allergen; allergic reaction; catalytic antibody;

XX target sequence.

OS Homo sapiens.

```

XX Key Location/Qualifiers
FH Region 181..257
FT /label="FcR binding region"
FT /note="residues 301-376 of IgE H chain, involved
FT Peptide 105..134
FT /note="target peptide I"
FT Peptide 193..225
FT /note="target peptide II"
PN US5258289-A.
PD 02-NOV-1993.
XX 05-SEP-1990; 90US-0577906.
XX 05-SEP-1990; 90US-0577906.
PR 05-SEP-1990; 90US-0577906.
PR 22-OCT-1991; 91US-0780765.
XX (DAVI/) DAVIS C G.
PI Davis CG, Fabian GR.
XX WPI; 1993-359735/45.
XX Selecting catalytic antibodies which cleave target peptide - used
XX to block allergic reactions or as preventive treatment
XX Example 2; Fig 3; 34pp; English.
XX Catalytic antibodies which cleave specific target sequences in the
XX IgE heavy chain constant region are exemplified. Cleavage is
XX targeted so as to separate the Fab (antigen binding region) from
XX the Fc region (contg. FcR binding site for attachment to the IgE
XX receptor on mast cells), thereby destroying receptor binding activity.
XX The target peptides were selected after consideration of their
XX primary and secondary structure. The antibodies can be used to block
XX allergic reactions.
SQ Sequence 428 AA;
Query Match 56.3%; Score 1723; DB 14; Length 428;
Best Local Similarity 77.7%; Pred. No. 9,3e-112;
Matches 345; Conservative 14; Mismatches 63; Indels 22; Gaps 7;
OY 129 REPQYVTLPPSRDELTKNOVSLT--CLYKGFPSDIAEWESNGCPENNYKTP-PVLD 185
DB 4 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMTWDT-GSLNGTMTLPTATLT 62
OY 186 VGSFELYKLYDKSRMOQGNFSCSVNHEALHNHYOORSLISPGKVEGGSGGSGS 245
DB 63 SGHYATISILTY-SCAMAK-QMFTCRVAH-----TSSSTWVNKTFEVC-----SV 104
OY 246 GGGSEFTPTPKYKILQSSCDGGGHPPTIOLCLVSGYTPGTINITWLEDGQVMDVLS 305
DB 105 CSRDFTPTPKYKILQSSCDGGGHPPTIOLCLVSGYTPGTINITWLEDGQVMDVLS 164
OY 306 TQEGELASTOSELTLSQKHWLSDRTYCOVYTGHTFEDSTKKCADSNPRGVSAYLSR 365
DB 165 TQEGELASTOSELTLSQKHWLSDRTYCOVYTGHTFEDSTKKCADSNPRGVSAYLSR 224
OY 366 PSFPLFTRKSPITITCLVVDLAPSKGTYNLTWSRAGKPVNHSRKEKORNGTLTVST 425
DB 225 PSFPLFTRKSPITITCLVVDLAPSKGTYNLTWSRAGKPVNHSRKEKORNGTLTVST 284
OY 426 LPVGRDMEIEGETYQCRVTHPHLPALMNSTKTSKGPRAAPEVYAFATPEWPGSRDKRTL 485
DB 285 LPVGRDMEIEGETYQCRVTHPHLPALMNSTKTSKGPRAAPEVYAFATPEWPGSRDKRTL 344
OY 486 CLIONFMPEDISVQMLHNEVOLPDARHSTQPRKTKSGGFVFSRLEVTTRAWEQKDEF 545
DB 345 CLIONFMPEDISVQMLHNEVOLPDARHSTQPRKTKSGGFVFSRLEVTTRAWEQKDEF 404

```

OY 546 CRAVHEAASPSQTVORAVSNPGK 569
 Db 405 CRAVHEAASPSQTVORAVSNPGK 428
 RESULT 7
 ID AU080284 standard; Protein: 323 AA.
 AC AU080284;
 DE 30-JUL-2002 (first entry)
 DE Human IGE heavy chain C2-C3-C4 domains.
 KW IGE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
 KW antihistaminic; dermatological; antiinflammatory; immunoglobulin E; IGE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 8..103 /note= "IGE heavy chain C2 domain"
 FT 100..114 /note= "Epitope including C2C3 linker"
 FT 104..111 /note= "Linker between domains C2 and C3"
 FT 112..211 /label= "IGE heavy chain C3 domain"
 FT 139..145 /note= "Epitope in BC loop"
 FT 167..175 /note= "Epitope in DE loop"
 FT 196..206 /note= "Epitope in FG loop"
 FT 210..218 /note= "Epitope including C3C4 linker"
 FT 212..215 /note= "Linker between domains C3 and C4"
 FT 216..317 /note= "IGE heavy chain C4 domain"
 FT Domain
 XX
 PN MO200220038-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 06-SEP-2001; 2001WO-DK00579.
 XX
 PR 06-SEP-2000; 2000DK-0001326.
 PR 15-SEP-2000; 2000US-232831P.
 XX
 PA (PHAR-) PHARMEXA AS.
 XX
 PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;
 DR WPI; 2002-383033/41.
 XX
 PT Inducing immune response against autologous immunoglobulin E in an
 PT animal, by effecting simultaneous presentation of cytotoxic T
 PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
 PT
 XX
 XX Disclosure; Page 105-106; 151pp; English.
 CC This invention relates to a novel method for inducing an immune response
 CC against autologous immunoglobulin E (IGE) in an animal. The method
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 CC (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell
 CC epitope (TH epitope) which is foreign to the animal, by antigen
 CC presenting cells (APCs) of the animal's immune system. The epitopes

CC of the invention may be used as a vaccine against allergic diseases. The
 CC method of the invention is useful for inducing an immune response
 CC against autologous IGE in an animal, which is useful for downregulating
 CC autologous IGE in the animal. This method is useful in the prevention
 CC and treatment of allergic diseases such as anaphylaxis, allergic
 CC rhinitis, asthma and atopic dermatitis. The present sequence represents
 CC the human IGE heavy chain C2-C3-C4 domains used to create the
 CC epitopes of the invention.
 XX
 XX Sequence 323 AA;
 SQ
 Query Match 55.8%; Score 1707; DB 23; Length 323;
 Best Local Similarity 100.0%; Pred. No. 8,4e-111;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 250 FTPTVKILQSSCGGGHFPPTIOLCLVSGYPTGTITITWLEQGVADVLDLSTASTTQ 309
 Db 4 FTPTVKILQSSCGGGHFPPTIOLCLVSGYPTGTITITWLEQGVADVLDLSTASTTQ 63
 OY 310 GELASTQSELTLSQKHWLSDRTYTCQVYVYQGHTEEDSTKCADSNPRGVSAVLSRPSFD 369
 Db 64 GELASTQSELTLSQKHWLSDRTYTCQVYVYQGHTEEDSTKCADSNPRGVSAVLSRPSFD 123
 OY 370 LFIKRSPTITCLVVDLAPSKGTVNLTWRSRAGKPVNHSRKEKQNRNGLTVTSLPGT 429
 Db 124 LFIKRSPTITCLVVDLAPSKGTVNLTWRSRAGKPVNHSRKEKQNRNGLTVTSLPGT 183
 OY 430 RDWIEGETYQCRVTHPHLPALMRSTYTSQPRAPAEYARATPEWPSRDKRTLACIQ 489
 Db 184 RDWIEGETYQCRVTHPHLPALMRSTYTSQPRAPAEYARATPEWPSRDKRTLACIQ 243
 OY 490 NFMPEEDISVOMLHNEVQLPDARHSTTOPRKTGSGFFVFSLEVTYRAEMQKDEFCRAV 549
 Db 244 NFMPEEDISVOMLHNEVQLPDARHSTTOPRKTGSGFFVFSLEVTYRAEMQKDEFCRAV 303
 OY 550 HEAASPSQTVORAVSNPGK 569
 Db 304 HEAASPSQTVORAVSNPGK 323
 RESULT 8
 ID AU080285 standard; Protein: 323 AA.
 AC AU080285;
 DE 30-JUL-2002 (first entry)
 DE Human IGE C2-C3-C4 domains for mammalian expression.
 KW IGE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
 KW antihistaminic; dermatological; antiinflammatory; immunoglobulin E; IGE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN MO200220038-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 06-SEP-2001; 2001WO-DK00579.
 XX
 PR 06-SEP-2000; 2000DK-0001326.
 PR 15-SEP-2000; 2000US-232831P.
 XX
 PA (PHAR-) PHARMEXA AS.
 XX
 PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;
 DR WPI; 2002-383033/41.
 DR N-PSDB; ABK51133.

XX Inducing immune response against autologous immunoglobulin E in an
PT animal, by effecting simultaneous presentation of cytotoxic T
PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
PT
XX
XX
PS Disclosure; Page 108-110; 151pp; English.
XX
CC This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (Ige) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes
CC of the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response
CC against autologous Ige in an animal, which is useful for downregulating
CC autologous Ige in the animal. This method is useful in the prevention
CC and treatment of allergic diseases such as anaphylaxis, allergic
CC rhinitis, asthma and atopic dermatitis. The present sequence represents
CC the human Ige heavy chain C2-C3-C4 domains optimised for expression in a
CC mammalian system, this sequence was used to create the epitopes of the
CC invention.
XX
XX Sequence 323 AA;
S0
Query Match 55.8%; Score 1707; DB 23; Length 323;
Best local similarity 100.0%; Pred. No. 8.4e-111;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 250 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEQGVMDVLDSTASTQ 309
DB 4 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEQGVMDVLDSTASTQ 63
QY 310 GELASTOSELTLSQKHWLSDRTYTCQVYQGHTEFDSRKCADSNPRGVSAVLSRPSFD 369
DB 64 GELASTOSELTLSQKHWLSDRTYTCQVYQGHTEFDSRKCADSNPRGVSAVLSRPSFD 123
QY 370 LFIKSPITITCLVNDLAPSKGTVNLTWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 429
DB 124 LFIKSPITITCLVNDLAPSKGTVNLTWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 183
QY 430 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPVYATATPEMPSRDKRTIACLIQ 489
DB 184 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPVYATATPEMPSRDKRTIACLIQ 243
QY 490 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFFVFSRLVETVRAMEQKDEFICRAV 549
DB 244 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFFVFSRLVETVRAMEQKDEFICRAV 303
QY 550 HEASPSQTVORAVSVNPGK 569
DB 304 HEASPSQTVORAVSVNPGK 323
RESULT 9
AAU80286
ID AAU80286 standard; Protein: 323 AA.
AC AAU80286;
XX
XX 30-JUL-2002 (first entry)
DE Human Ige C2-C3-C4 domains for E.Coli expression.
XX
KM Ige; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
KM antilasthmatic; dermatological; antinflammatory; immunoglobulin E; Ige;
KM vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KM heavy chain C domain.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN W0200220038-A2.
XX
XX 14-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-DK00579.
XX
XX 06-SEP-2000; 2000DK-0001326.
PR 15-SEP-2000; 2000US-232831P.
XX
XX (PHAR-) PHARMEXA AS.
XX
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX WPI: 2002-383033/41.
DR N-PSDB: ABK51134.
XX
XX Inducing immune response against autologous immunoglobulin E in an
PT animal, by effecting simultaneous presentation of cytotoxic T
PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
PT
XX
XX Disclosure; Page 112-113; 151pp; English.
XX
CC This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (Ige) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes
CC of the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response
CC against autologous Ige in an animal, which is useful for downregulating
CC autologous Ige in the animal. This method is useful in the prevention
CC and treatment of allergic diseases such as anaphylaxis, allergic
CC rhinitis, asthma and atopic dermatitis. The present sequence represents
CC the human Ige heavy chain C2-C3-C4 domains optimised for expression in
CC the human system, this sequence was used to create the epitopes of the
CC invention.
XX
XX Sequence 323 AA;
S0
Query Match 55.8%; Score 1707; DB 23; Length 323;
Best local similarity 100.0%; Pred. No. 8.4e-111;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 250 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEQGVMDVLDSTASTQ 309
DB 4 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEQGVMDVLDSTASTQ 63
QY 310 GELASTOSELTLSQKHWLSDRTYTCQVYQGHTEFDSRKCADSNPRGVSAVLSRPSFD 369
DB 64 GELASTOSELTLSQKHWLSDRTYTCQVYQGHTEFDSRKCADSNPRGVSAVLSRPSFD 123
QY 370 LFIKSPITITCLVNDLAPSKGTVNLTWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 429
DB 124 LFIKSPITITCLVNDLAPSKGTVNLTWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 183
QY 430 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPVYATATPEMPSRDKRTIACLIQ 489
DB 184 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPVYATATPEMPSRDKRTIACLIQ 243
QY 490 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFFVFSRLVETVRAMEQKDEFICRAV 549
DB 244 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFFVFSRLVETVRAMEQKDEFICRAV 303
QY 550 HEASPSQTVORAVSVNPGK 569
DB 304 HEASPSQTVORAVSVNPGK 323
RESULT 10
AAR83559
ID AAR83559 standard; Protein: 324 AA.

```

XX AAR83559;
AC 06-MAR-1996 (first entry)
DT XX
DE Fc(epsilon) CH2'-CH4 protein sequence.
XX
KM Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
KW constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
KV histamine; anti-allergenic; vaccine; immune response.
XX
OS Synthetic.
XX FR2715304-A1.
XX
PD 28-JUL-1995.
XX
PE 26-JAN-1994; 94FR-0000846.
XX
PR 26-JAN-1994; 94FR-0000846.
XX
PA (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
XX
PI Hurpin CM, Panero MJM;
XX WPI: 1995-265243/35.
XX N-PSDB; AAT01865.
XX
PT Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain
PT - has epitope(s) not present in native IgE, also derived antibodies
PT for treating or preventing allergies, inflammatory immune disease,
PT etc.
XX
PS Claim 3; Page 32-33; 44pp; French.
XX
XX The amino acid sequence of the Fc(epsilon) CH2'-CH4 fragment covering
CC amino acids 226-547. The DNA sequence was isolated from a human myeloma
CC 266BL cDNA library screened with a probe corresp. to the N-terminus of
CC IGE. The region encoding amino acids 218-547 was cloned into the vector
CC pMT211 under control of the tryptophan promoter. The resultant protein
CC produced contains some non-Fc amino acids. These were removed by
CC replacing their coding sequence with a bicistronic linker. The resultant
CC construct encodes the Fc(epsilon) constant heavy region from amino acids
CC 226-547. When it is expressed in E.coli, the protein produced is a
CC non-glycosylated Fc(epsilon) fragment. Altering the pattern of
CC glycosylation unmasks new antigenic sites thus rendering the Fc fragment
CC immunogenic and able to induce antibodies that recognise native IgE but
CC do not form histamine-releasing complexes. The Fc fragments can be used
CC in anti-allergic vaccines to modulate the intensity of immune responses
CC mediated by IgE.
XX
SQ Sequence 324 AA;
Query Match 55.8%; Score 1707; DB 16; Length 324;
Best Local Similarity 100.0%; Pred. No. 8.5e-111;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 490 NFMPEDISVQWLNHNEVQLPDARHSTTPRKTKSGGFFVFSRLVETRAEMQKDEFTICRAV 549
DB 245 NFMPEDISVQWLNHNEVQLPDARHSTTPRKTKSGGFFVFSRLVETRAEMQKDEFTICRAV 304
OY 550 HEASPQOTVORAVSVNPGK 569
DB 305 HEASPQOTVORAVSVNPGK 324
RESULT 11
AAR75225 ID AAR75225 standard; Protein: 325 AA.
XX
AC AAR75225;
XX
DT 10-NOV-1995 (first entry)
XX
DE Human IgE Fc chain (amino acids 224-547) mutant sequence.
XX
KM IgE Fc fragment; antiallergic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 149 /label= Asn371
FT /note= "glycosylation site"
FT Misc-difference 172 /label= Asn394
FT /note= "glycosylation site"
FT Misc-difference 1 /label= Val224
FT /note= "any AA or deletion"
FT Misc-difference 2 /label= Cys225
FT /note= "Ala, any other AA, or deletion"
FT Misc-difference 3 /label= Ser226
FT /note= "any AA or deletion"
FT Misc-difference 4 /label= Arg227
FT /note= "any AA or deletion"
FT Misc-difference 5 /label= Asp228
FT /note= "any AA or deletion"
XX
XX WO9514779-A.
XX
XX 01-JUN-1995.
XX
XX 22-NOV-1994; 94WO-GB02561.
XX
XX 22-NOV-1993; 93GB-0024013.
XX
XX (THRE-) 3I RES EXPL LTD.
XX (CLUT ) CELUTECH THERAPEUTICS LTD.
XX
XX Gould HJ, Owens RJ, Sutton BJ, Young RJ;
XX WPI: 1995-206936/27.
XX N-PSDB; AA087474.
XX
XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc
XX useful to study and treat allergy.
XX
XX Disclosure; Page 6; 55pp; English.
XX
XX The sequence represents a mutant sequence of a human IgE-Fc
XX chain (amino acids 224-547) which is of sufficient length to bind
XX Fc-epsilon RI and/or Fc-epsilon FcRI IgE receptor sites on human
XX cells. The protein is useful in the study and treatment of
XX allergy.
XX

```


SQ Sequence 325 AA;

Query Match	55.8%	Score 1707;	DB 16;	Length 325;
Best Local Similarity	100.0%	Pred. No. 8.5e-11;		
Matches 320;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	250	FPPPYKLIQSSCDGGHPPIIOLCLVSGTPTIINILEGQVMDVLSASTJOE	309
Db	6	FPPPYKLIQSSCDGGHPPIIOLCLVSGTPTIINILEGQVMDVLSASTJOE	65
Qy	310	GELASTQSELISOKHMLSDRTTYOVTYQGHTEPDSKKCADSNPGVSATILSRPSPD	369
Db	66	GELASTQSELISOKHMLSDRTTYOVTYQGHTEPDSKKCADSNPGVSATILSRPSPD	1255
Qy	370	LFIKRSPTITCLVNDLAPSKGTVNLTWBRASGKPVNHSTRKEERONGTLTVSTLPVGT	429
Db	126	LFIKRSPTITCLVNDLAPSKGTVNLTWBRASGKPVNHSTRKEERONGTLTVSTLPVGT	185
Qy	430	RDMIIEETTYQCRVTHPLPRALMRSTYTSQGPRAPEVYATPATEWFGSRDKTTLACLIQ	489
Db	186	RDMIIEETTYQCRVTHPLPRALMRSTYTSQGPRAPEVYATPATEWFGSRDKTTLACLIQ	245
Qy	490	NFMPEBISYQWMLHNEVOLDPAHRSHTQRTKGSSEFYSRLTYRAWEQKDEFCICRAV	549
Db	246	NFMPEBISYQWMLHNEVOLDPAHRSHTQRTKGSSEFYSRLTYRAWEQKDEFCICRAV	305
Qy	550	HEAASPSQTVQRAVSYNPGK	569
Db	306	HEAASPSQTVQRAVSYNPGK	325

RESULT 12
AAR77241
ID AAR77241 standard; Protein; 325 AA.

AC AAR77241;

DT 10-NOV-1995 (first entry)

Human IgE Fc chain (amino acids 224-547) wild-type sequence.

IgE Fc fragment; antiallergic.

05 Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
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100	100	100

/label= Asn371

FT Misc-difference 172

/note= "glycosylation site"

PN W09514779-A.

PD 01-JUN-1995

PF 22-NOV-1994; 94WO-GB02561.

PR 22-NOV-1993; 93GB-0024013.

PA (THRE-) 3I RES EXPL LTD.

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EUNT: 1005 206036 207

DR N-PSDB; AAQ91170.

PT Mutated glycosylase

[illegible]

XX The sequence represents the wild-type sequence of a human IgE-Fc
 CC chain (amino acids 224-547) which is of sufficient length to bind
 CC Fc-epsilon RI and/or Fc-epsilon RI Fc receptor sites on human
 CC cells. The sequence is preferably mutated (see AAR75223) to
 CC represent a protein encoding a protein where Cys225 is mutated,
 CC optionally together with Val224, Ser226 and Arg227. The protein
 CC is useful in the study and treatment of allergy.
 XX
 SO Sequence 325 AA:

SQ Sequence 325 AA;

Query Match	55.8%	Score 1707	DB 16	Length 325
Best Local Similarity	100.0%	Pred. No. 8.5e-111		
Matches 320	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy	250	FTPTVTKLOS	CGGGGHEPPTIQLLCVSYGTGNTIWL	EGQVMDVLS	ASTAQOE	309		
Db	6	FTPTVTKLOS	CGGGGHEPPTIQLLCVSYGTGNTIWL	EGQVMDVLS	ASTAQOE	65		
Oy	310	GELASTOSELT	LSOKHMLS	DRTYTCQVYTGHTFEDSTK	KCADSNPRGSAYLSRPSPD	369		
Db	66	GELASTOSELT	LSOKHMLS	DRTYTCQVYTGHTFEDSTK	KCADSNPRGSAYLSRPSPD	125		
Oy	370	LFIRKSPIT	TLVVDLAPSK	TVMLTWSRAGSKPVNHSTRKEE	KORNTLTVSTLPGT	429		
Db	126	LFIRKSPIT	TLVVDLAPSK	TVMLTWSRAGSKPVNHSTRKEE	KORNTLTVSTLPGT	185		
Oy	430	RDWIEGET	YOCRVTHPHIL	PRALMRS	STKTSQPRAP	EVYAFATPBM	PGSRDKRTLACIQ	489
Db	186	RDWIEGET	YOCRVTHPHIL	PRALMRS	STKTSQPRAP	EVYAFATPBM	PGSRDKRTLACIQ	245
Oy	490	NFMEDIS	QVCLNHN	EVOLPDR	HNSTORPKTKGSGFEVSR	LEVTYRAEM	QKDEFICAV	549
Db	246	NFMEDIS	QVCLNHN	EVOLPDR	HNSTORPKTKGSGFEVSR	LEVTYRAEM	QKDEFICAV	305
Oy	550	HEAASPSQ	TVQRAV	SVNPGK	569			
Db	306	HEAASPSQ	TVQRAV	SVNPGK	325			

RESULT 13

ID AAB03642 standard; protein; 331 AA.

AC AAB03642

DT 22-NOV-2000 (first entry)

DE Human IgE heavy chain constant regions 2, 3 and 4.

KW Human; immunoglobulin E; IgE; vaccination; infection; allergy;

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PR 22-SEP-1999; 99US-0401636

PA (RESI-) RESISTENTIA PHARM AB.

PI Helman LT;

DR WPI; 2000-365342/31

PT Immunogenic polypeptides useful for preventing the harmful effects of

PS Disclosure: Fig 1: 50pp: English.

CC The present sequence is an immunogenic peptide consisting of the
CC heavy chain constant regions 2, 3 and 4 of the human IGE. It was used to
CC construct a number of immunogenic peptides which consisted of regions of
CC IGE from different mammals, which appear to cause a stronger polyclonal
CC anti-self IGE response than peptides consisting of the same regions from
CC one mammal. Immunogenic peptides, particularly those consisting of
CC different heavy chain constant regions, can be used for vaccination
CC in humans, against bacterial and viral infections and allergies, such
CC as asthma, fur, pollen and food allergies and eczema.

XX Sequence 331 AA;

Query Match 55.8%; Score 1707; DB 21; Length 331;

Best Local Similarity 100.0%; Pred. No. 8.7e-111;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 FTPTVVKILQSSCGGHHFPTIQLCLVSGTYTGTTINITWLEGGQVMDVLDLSTASTQOE 309
DB 12 FTPTVVKILQSSCGGHHFPTIQLCLVSGTYTGTTINITWLEGGQVMDVLDLSTASTQOE 71
QY 310 GELASTOSELTLSQKHMLSDRTYTCQVYTGHTFEDSTKCKADSNPRGVSAYLSRPSFDP 369
DB 72 GELASTOSELTLSQKHMLSDRTYTCQVYTGHTFEDSTKCKADSNPRGVSAYLSRPSFDP 131
QY 370 LPIKRSPTITCLVVDLAPSKGTVNLWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 429
DB 132 LPIKRSPTITCLVVDLAPSKGTVNLWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 191
QY 430 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAPEYAAATPEWPGSRKRTLACLIQ 489
DB 192 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAPEYAAATPEWPGSRKRTLACLIQ 251
QY 490 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFVFSRLLEYTRAEMQKDEFICRAV 549
DB 252 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFVFSRLLEYTRAEMQKDEFICRAV 311
QY 550 HEAASPSQTVORAVSVNPGK 569
DB 312 HEAASPSQTVORAVSVNPGK 331

RESULT 14

AAP80291
ID AAP80291 standard; protein: 367 AA.

XX AAP80291;

DT 06-DEC-1990 (first entry)

DE Interleukin-2/IgE Fc fusion protein.

KW Interleukin-2; IGE Fc receptor; fusion protein; asthma; dermatitis.

XX synthetic.

OS Key

FT Peptide 1..20 Location/Qualifiers

FT Peptide 21..31 /label=IL-2 leader sequence

FT Peptide 32..36 /label=IL-2 N-terminal

FT Peptide 37..367 /label=linker

XX Peptide

XX EP269455-A.

XX 01-JUN-1988.

XX 27-NOV-1987; 87EP-0310475.

XX 18-SEP-1987; 87JP-0232295.

PR 28-NOV-1986; 86JP-0281871.

XX (TAKE) TAKEDA CHEMICAL IND KK.

XX Ikeyama S, Nishimura O;

XX WPI: 1986-149211/22.

PR Fused protein for allergy treatment - comprising interleukin-2

PT N-terminal residues, a linker and human immunoglobulin E Fc

PT fragment.

XX This fusion protein has a low toxicity and is useful in therapy

XX for allergy induced by IGE. It can be used in the treatment of

XX allergic dermatosis, atopic dermatitis or bronchial asthma.

XX Sequence 367 AA;

Query Match 55.8%; Score 1707; DB 9; Length 367;

Best Local Similarity 100.0%; Pred. No. 9.9e-111;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 FTPTVVKILQSSCGGHHFPTIQLCLVSGTYTGTTINITWLEGGQVMDVLDLSTASTQOE 309
DB 48 FTPTVVKILQSSCGGHHFPTIQLCLVSGTYTGTTINITWLEGGQVMDVLDLSTASTQOE 107
QY 310 GELASTOSELTLSQKHMLSDRTYTCQVYTGHTFEDSTKCKADSNPRGVSAYLSRPSFDP 369
DB 108 GELASTOSELTLSQKHMLSDRTYTCQVYTGHTFEDSTKCKADSNPRGVSAYLSRPSFDP 167
QY 370 LPIKRSPTITCLVVDLAPSKGTVNLWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 429
DB 168 LPIKRSPTITCLVVDLAPSKGTVNLWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 227
QY 430 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAPEYAAATPEWPGSRKRTLACLIQ 489
DB 228 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAPEYAAATPEWPGSRKRTLACLIQ 287
QY 490 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFVFSRLLEYTRAEMQKDEFICRAV 549
DB 288 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFVFSRLLEYTRAEMQKDEFICRAV 347
QY 550 HEAASPSQTVORAVSVNPGK 569
DB 348 HEAASPSQTVORAVSVNPGK 367

RESULT 15

AA79994
ID AA79994 standard; Protein: 325 AA.

XX AA79994;

DT 15-MAY-2000 (first entry)

DE Human immunoglobulin E epsilon heavy chain SEQ ID NO:1.

KW Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Homo sapiens.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA Wang CY, Walfield AM;

PI WPI: 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy

XX Example 1; Page 66-68; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC and anti-asthmatic properties. (I) induces polyclonal antibodies
CC specific for a target effector site on the epsilon-heavy chain of IgE,
CC and so preventing triggering and activation of mast cells and basophils
CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe
CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino
CC acid sequences used in the exemplification of the present invention.

XX Sequence 325 AA:

Query Match 55.6%; Score 1701; DB 21; Length 325;

Best Local Similarity 99.4%; Pred. No. 2,2e-110;

Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 250 FTPTVKILQSSCDGGHFPPTIQLCLVSGYPTGTINITWLEGGQVMDVLISTASTQOE 309
DB 6 FTPTVKILQSSCDGGHFPPTIQLCLVSGYPTGTINITWLEGGQVMDVLISTASTQOE 65
OY 310 GELASTOSELTLSQKHMISDRYTCQVYQGHTEFEDSTKCKADSNPRGVSAIISRSPFD 369
DB 66 GELASTOSELTLSQKHMISDRYTCQVYQGHTEFEDSTKCKADSNPRGVSAIISRSPFD 125
OY 370 LFIKSPITITCLVNDLAPSKGTNLTWMSRASKPVNHSTRKEKQNGTLVYTSILPYGT 429
DB 126 LFIKSPITITCLVNDLAPSKGTNLTWMSRASKPVNHSTRKEKQNGTLVYTSILPYGT 185
OY 430 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAPEVYAFATPEMPGSRDKRTLACLIQ 489
DB 186 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAPEVYAFATPEMPGSRDKRTLACLIQ 245
OY 490 NFMPEIDISVQMLHNEVQLPDARHSTQPRKTKGSGFFVSRLEVTRAEMEQDEFICRAV 549
DB 246 NFMPEIDISVQMLHNEVQLPDARHSTQPRKTKGSGFFVSRLEVTRAEMEQDEFICRAV 305
OY 550 HEAASPQOTVORAVSVNPGK 569
DB 306 HEAASPQOTVORAVSVNPGK 325

Search completed: July 15, 2003, 06:57:41
Job time : 68.0009 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: July 15, 2003, 06:59:40 ; Search time 43.6521 Seconds
(without alignments)
1517.518 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDKHTHPCPCAPPELL.....HEAASPTQVRAVSVPNGK 569

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCIT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCITUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3060	100.0	569	US-09-847-208-7	Sequence 7, Appl1
2	1775	58.0	574	US-10-047-542-45	Sequence 45, Appl1
3	1775	58.0	574	US-10-214-524-37	Sequence 37, Appl1
4	1766	57.7	427	US-09-847-208-5	Sequence 6, Appl1
5	1766	57.7	428	US-10-047-542-60	Sequence 60, Appl1
6	1766	57.7	428	US-09-949-375A-1	Sequence 1, Appl1
7	1766	57.4	491	US-09-916-230-1	Sequence 1, Appl1
8	1755	57.4	542	US-09-949-375A-7	Sequence 7, Appl1
9	1729	56.5	592	US-10-207-655-334	Sequence 334, App
10	1707	55.8	320	US-09-847-208-6	Sequence 6, Appl1
11	1707	55.8	323	US-09-949-375A-2	Sequence 2, Appl1
12	1707	55.8	323	US-09-949-375A-4	Sequence 4, Appl1
13	1707	55.8	323	US-09-949-375A-6	Sequence 6, Appl1
14	1707	55.8	331	US-10-176-664-1	Sequence 1, Appl1
15	1707	55.8	331	US-10-207-655-339	Sequence 329, App
16	1707	55.8	331	US-09-401-636-1	Sequence 1, Appl1
17	1705.5	55.7	426	US-10-214-524-26	Sequence 26, Appl1
18	1696	55.4	336	US-09-949-375A-8	Sequence 8, Appl1
19	1671	54.6	330	US-09-949-375A-10	Sequence 10, Appl1

20	1649	53.9	347	9	US-10-152-190-13	Sequence 13, Appl1
21	1579	51.6	347	9	US-10-152-190-12	Sequence 12, Appl1
22	1566.5	51.2	348	9	US-10-152-190-11	Sequence 11, Appl1
23	1435.5	46.9	346	9	US-10-152-190-10	Sequence 10, Appl1
24	1364.5	44.6	346	9	US-10-152-190-14	Sequence 14, Appl1
25	1273.5	41.6	711	9	US-10-071-485-90	Sequence 90, Appl1
26	1260	41.2	232	9	US-09-847-208-3	Sequence 3, Appl1
27	1260	41.2	330	9	US-09-847-208-2	Sequence 2, Appl1
28	1234.5	40.3	731	10	US-09-825-012-46	Sequence 46, Appl1
29	1234.5	40.3	741	10	US-09-825-012-55	Sequence 55, Appl1
30	1232	40.3	660	9	US-10-294-055-8	Sequence 8, Appl1
31	1227	40.1	543	9	US-10-207-655-345	Sequence 345, App
32	1225	40.0	232	10	US-09-996-357-10	Sequence 10, Appl1
33	1225	40.0	235	9	US-10-207-655-208	Sequence 208, App
34	1225	40.0	247	10	US-09-996-357-13	Sequence 13, Appl1
35	1225	40.0	251	9	US-10-008-063-18	Sequence 18, Appl1
36	1225	40.0	251	9	US-10-152-363A-6	Sequence 6, Appl1
37	1225	40.0	267	10	US-09-996-357-12	Sequence 12, Appl1
38	1225	40.0	288	9	US-09-822-851B-14	Sequence 14, Appl1
39	1225	40.0	288	9	US-10-119-637A-14	Sequence 14, Appl1
40	1225	40.0	330	9	US-10-047-542-20	Sequence 20, Appl1
41	1225	40.0	330	9	US-09-995-898A-15	Sequence 15, Appl1
42	1225	40.0	330	9	US-09-892-949-38	Sequence 38, Appl1
43	1225	40.0	330	9	US-10-269-805-68	Sequence 68, Appl1
44	1225	40.0	331	9	US-10-341-836-2	Sequence 2, Appl1
45	1225	40.0	332	9	US-09-990-586-98	Sequence 98, Appl1

ALIGNMENTS

RESULT 1

US-09-847-208-7
Sequence 7, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847.208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 569
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
US-09-847-208-7

Query Match 100.0%: Score 3060; DB 9; Length 569;
Best Local Similarity 100.0%: Pred. No. 8.5e-181;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EKSCDKHTHPCPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVYVDSHEDPEVKF	60
DB	1	EKSCDKHTHPCPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVYVDSHEDPEVKF	60
QY	61	NMVYGVGEVHNKTKPREQYNSTYRVYSLVTLVHQNMNGEKYCKSNALPAPIKT	120
DB	61	NMVYGVGEVHNKTKPREQYNSTYRVYSLVTLVHQNMNGEKYCKSNALPAPIKT	120
QY	121	ISKAVQPREPOVYITLPSRDELTKNQVSTICFLYGFPSDIAVEMESNGQPENNYKTTT	180
DB	121	ISKAVQPREPOVYITLPSRDELTKNQVSTICFLYGFPSDIAVEMESNGQPENNYKTTT	180
QY	181	PVLDSVGSFFLYSKLTVDKSRMQQGNVSCSYMHDLNHNQOQSLSLSPCKVEGSGGSG	240
DB	181	PVLDSVGSFFLYSKLTVDKSRMQQGNVSCSYMHDLNHNQOQSLSLSPCKVEGSGGSG	240

Db 181 PVLDSVGSFLLSKRLTVDKSRMOQNVFSCVMHEALNHNHVOQRSLSPGKVEGGSG 240
Qy 241 GGGSGGGGFTPPYKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDDGVMD 300
Db 241 GGGSGGGGFTPPYKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDDGVMD 300
Qy 301 LSTASTOEGELASTOSELTSOKHMLSRTYTCOVYOGHFFEDSTKCKADSNRGSA 360
Db 301 LSTASTOEGELASTOSELTSOKHMLSRTYTCOVYOGHFFEDSTKCKADSNRGSA 360
Qy 361 YLSRSPEDFLIRKSPITITCLVNDLAPSKGTYNLWMSASGKPVNHSRKEKQNGTLY 420
Db 361 YLSRSPEDFLIRKSPITITCLVNDLAPSKGTYNLWMSASGKPVNHSRKEKQNGTLY 420
Qy 421 VTSLPVGTDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEWGSRD 480
Db 421 VTSLPVGTDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEWGSRD 480
Qy 481 KRTIACLIOMFPEDISYQWLHNEVQLPDARHSTTOPRKTGSGFFVSRLLEVTRAEMQ 540
Db 481 KRTIACLIOMFPEDISYQWLHNEVQLPDARHSTTOPRKTGSGFFVSRLLEVTRAEMQ 540
Qy 541 KDEFICRAVHEAASPSQTVORAVSNPGK 569
Db 541 KDEFICRAVHEAASPSQTVORAVSNPGK 569

RESULT 2
US-10-047-542-45

Sequence 45, Application US/10047542
Patent No. US20020168367A1
GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WICOF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
FILE REFERENCE: 030905.0004.C1P1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-10-047-542-45

Query Match 58.0%; Score 1775; DB 9; Length 574;
Best Local Similarity 77.3%; Pred. No. 1.1e-101;
Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

Qy 120 TISAKVOPRPOYYTLPSRDELTKNOVSLT--CLVKGYPDSIAVWESNGPENNYK 177
Db 143 TVSSASTQ--SPSYFPLTRCKKNIPSNATSVTLGLATGYPPEVWMTWDT--GSLNGTMM 199
Qy 178 TTP-PVLDSVGSFLLSKRLTVDKSRMOQNVFSCVMHEALNHNH--QORSLSLPGKVEG 235
Db 200 TLPATITLISGHVATISLTV--SGAMAK--QMFTCRVAHFTSSDWMVNKTFEVC----- 251
Qy 236 GGGSGGGGSGGSGFTPPYKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDDQ 295
Db 252 -----SRGFTPPYKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDDQ 300
Qy 296 VMDVLDSTASTOEGELASTOSELTSOKHMLSRTYTCOVYOGHFFEDSTKCKADSNP 355
Db 301 VMDVLDSTASTOEGELASTOSELTSOKHMLSRTYTCOVYOGHFFEDSTKCKADSNP 360
Qy 356 RGVSAVLSRSPEDFLIRKSPITITCLVNDLAPSKGTYNLWMSASGKPVNHSRKEKOR 415
Db 356 RGVSAVLSRSPEDFLIRKSPITITCLVNDLAPSKGTYNLWMSASGKPVNHSRKEKOR 415

Db 361 RGVSAVLSRSPEDFLIRKSPITITCLVNDLAPSKGTYNLWMSASGKPVNHSRKEKOR 420
Qy 416 NGTLVTVSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEW 475
Db 421 NGTLVTVSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEW 480
Qy 476 PGSDKRTIACLIOMFPEDISYQWLHNEVQLPDARHSTTOPRKTGSGFFVSRLLEVTR 535
Db 481 PGSDKRTIACLIOMFPEDISYQWLHNEVQLPDARHSTTOPRKTGSGFFVSRLLEVTR 540
Qy 536 AEMQKDEFICRAVHEAASPSQTVORAVSNPGK 569
Db 541 AEMQKDEFICRAVHEAASPSQTVORAVSNPGK 574

RESULT 3
US-10-214-524-37

Sequence 37, Application US/10214524
Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Swei-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REFERENCE: 168-00101.P.1.1
CURRENT FILING DATE: 2002-08-08
CURRENT APPLICATION NUMBER: US/10/214,524
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 574
TYPE: PRT
ORGANISM: Human (Homo sapiens)
US-10-214-524-37

Query Match 58.0%; Score 1775; DB 9; Length 574;
Best Local Similarity 77.3%; Pred. No. 1.1e-101;
Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

Qy 120 TISAKVOPRPOYYTLPSRDELTKNOVSLT--CLVKGYPDSIAVWESNGPENNYK 177
Db 143 TVSSASTQ--SPSYFPLTRCKKNIPSNATSVTLGLATGYPPEVWMTWDT--GSLNGTMM 199
Qy 178 TTP-PVLDSVGSFLLSKRLTVDKSRMOQNVFSCVMHEALNHNH--QORSLSLPGKVEG 235
Db 200 TLPATITLISGHVATISLTV--SGAMAK--QMFTCRVAHFTSSDWMVNKTFEVC----- 251
Qy 236 GGGSGGGGSGGSGFTPPYKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDDQ 295
Db 252 -----SRGFTPPYKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDDQ 300
Qy 296 VMDVLDSTASTOEGELASTOSELTSOKHMLSRTYTCOVYOGHFFEDSTKCKADSNP 355
Db 301 VMDVLDSTASTOEGELASTOSELTSOKHMLSRTYTCOVYOGHFFEDSTKCKADSNP 360
Qy 356 RGVSAVLSRSPEDFLIRKSPITITCLVNDLAPSKGTYNLWMSASGKPVNHSRKEKOR 415
Db 361 RGVSAVLSRSPEDFLIRKSPITITCLVNDLAPSKGTYNLWMSASGKPVNHSRKEKOR 420
Qy 416 NGTLVTVSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEW 475
Db 421 NGTLVTVSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEW 480
Qy 476 PGSDKRTIACLIOMFPEDISYQWLHNEVQLPDARHSTTOPRKTGSGFFVSRLLEVTR 535
Db 481 PGSDKRTIACLIOMFPEDISYQWLHNEVQLPDARHSTTOPRKTGSGFFVSRLLEVTR 540
Qy 536 AEMQKDEFICRAVHEAASPSQTVORAVSNPGK 569
Db 541 AEMQKDEFICRAVHEAASPSQTVORAVSNPGK 574

Query Match	57.7%;	Score 1766;	DB 9;	Length 427;
Best Local Similarity	78.0%;	Pred. NO. 2.8e-101;		
Matches 347;	Conservative 17;	Mismatches 57;	Indels 24;	Gaps 7;

RESULT 5
US-10-047-542-60
; Sequence 60, Application US/10047542
; Patent No. US20020168367A1

QY	DB	Sequence	Score	DB %	Length	Mismatches	Indels	Gaps
QY	Db	129 REPQYVILPPSRDELTKNQVSLT-CLVKGFPYSDIAEVESNGCPENNYKTP-PVLDS	57.7%	1766;	428;	7	24	7
QY	Db	4 QSPVFPFLTRCKKINPSNATSVTLGCLATGYFPEPVMTWDT-GSLNGTMTLPTTLL	78.0%	Pred. No. 2.8e-101;				
QY	Db	186 VGSFELSKLTVDKSRMOGVNFCSCVMHEALHNHY-QORSLSLSPKVEGGGSGGGGS						
QY	Db	63 SGHATISLTLV-SGAMAK-QMFCRVAHFTSSTWVYKNTFSVC-----						
QY	Db	245 GGGSGFTPTPVKIIQSSCDGGGHPPTIQLCLVSGVYPGTINITWLEDGQYMDVLS						
QY	Db	106 --SRDFPTPVKIIQSSCDGGGHPPTIQLCLVSGVYPGTINITWLEDGQYMDVLS						
QY	Db	305 STQEGELASQSELTLSQKHWLSRQYTCQVYQGHFEEDSTKCADSNPVSAYLSR						
QY	Db	164 STQEGELASQSELTLSQKHWLSRQYTCQVYQGHFEEDSTKCADSNPVSAYLSR						
QY	Db	365 PSPEDLFRKSPITICLVVDLAPSKGYNLTWMSRAGKPVNHSRTRKEEKORNGTLVTST						
QY	Db	224 PSPEDLFRKSPITICLVVDLAPSKGYNLTWMSRAGKPVNHSRTRKEEKORNGTLVTST						
QY	Db	425 LPVGRDRIIEGETYQCRVTHHPLRALMRSTTKTSGPRAAPVYAFATPEWGSRDRTL						
QY	Db	284 LPVGRDRIIEGETYQCRVTHHPLRALMRSTTKTSGPRAAPVYAFATPEWGSRDRTL						
QY	Db	485 AQLIENFPEIDISVQMLNEVQLPDARHSTQPRKTKSGGFVEFRLLEYTRAWEQKDEF						
QY	Db	344 AQLIENFPEIDISVQMLNEVQLPDARHSTQPRKTKSGGFVEFRLLEYTRAWEQKDEF						
QY	Db	545 ICRVHFAASPSQTVQRAVSNPGK						
QY	Db	404 ICRVHFAASPSQTVQRAVSNPGK						


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OY 462 RAAPVYAFATPEWPGSDKRTLACLIONFMPEDISVOMLHNEVOLDPARHSTTOPRRTK 521
:
:
:
DB 485 RAAPVYAFATPEWPGSDKRTLACLIONFMPEDISVOMLHNEVOLDPARHSTTOPRRTK 544
:
:
:
OY 522 GSGFFVFSRLLEVTRAEMWOKDEFICRAVHEAASPSQTVORAVSNPGK 569
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DB 545 GSGFFVFSRLLEVTRAEMWOKDEFICRAVHEAASPSQTVORAVSNPGK 592
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:
:
RESULT 10
US-09-847-208-6
: Sequence 6, Application US/09847208
: Publication No. US20030082190A1
: GENERAL INFORMATION:
: APPLICANT: Saxon, Andrew
: APPLICANT: Zhang, Ke
: APPLICANT: Zhu, Daocheng
: TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
: TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
: FILE REFERENCE: US67,002A
: CURRENT APPLICATION NUMBER: US/09/847,208
: CURRENT FILING DATE: 2001-05-01
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 320
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-847-208-6

Query Match 55.8%; Score 1707; DB 9; Length 320;
Best Local Similarity 100.0%; Pred. No. 8.9e-96;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 FTPTVKILQSSCGGHHFPTIOLCLVSGYTPGTINITIWLLEDQYMDVLDLSTASTOE 309
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:
:
DB 1 FTPTVKILQSSCGGHHFPTIOLCLVSGYTPGTINITIWLLEDQYMDVLDLSTASTOE 60
:
:
:
OY 310 GELASTOSELTLSQKHWLSDRTYTCQVYGGHTEFEDSTKCADSNPBGVAYLSRPSFD 369
:
:
:
DB 61 GELASTOSELTLSQKHWLSDRTYTCQVYGGHTEFEDSTKCADSNPBGVAYLSRPSFD 120
:
:
:
OY 370 LFIKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEEQRNGTLTVSTLPVGT 429
:
:
:
DB 121 LFIKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEEQRNGTLTVSTLPVGT 180
:
:
:
OY 430 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPVYAFATPEWPGSDKRTLACLIO 489
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:
:
DB 181 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPVYAFATPEWPGSDKRTLACLIO 240
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:
OY 490 NFMEDISVOMLHNEVOLDPARHSTTOPRRTKSGGFFVFSRLLEVTRAEMWOKDEFICRAV 549
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DB 241 NFMEDISVOMLHNEVOLDPARHSTTOPRRTKSGGFFVFSRLLEVTRAEMWOKDEFICRAV 300
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OY 550 HEAASPSQTVORAVSNPGK 569
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DB 301 HEAASPSQTVORAVSNPGK 320
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RESULT 11
US-09-949-375A-2
: Sequence 2, Application US/09949375A
: Patent No. US2002017267A1
: GENERAL INFORMATION:
: APPLICANT: KLYSNER, Steen et al.
: TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
: FILE REFERENCE: 3631-0111P
: CURRENT APPLICATION NUMBER: US/09/949,375A
: CURRENT FILING DATE: 2002-01-18
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
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:
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:
: LENGTH: 323
: TYPE: PRT
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (8)..(103)
: OTHER INFORMATION: Human Ige heavy chain C2 domain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (112)..(211)
: OTHER INFORMATION: Human Ige heavy chain C3 domain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (216)..(317)
: OTHER INFORMATION: Human Ige heavy chain C4 domain
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (104)..(111)
: OTHER INFORMATION: Linker between domains C2 and C3
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (212)..(215)
: OTHER INFORMATION: Linker between domains C3 and C4
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (100)..(114)
: OTHER INFORMATION: Epitope including C2C3 linker
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (210)..(218)
: OTHER INFORMATION: Epitope including C3C4 linker
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (139)..(145)
: OTHER INFORMATION: Epitope in BC loop
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (167)..(175)
: OTHER INFORMATION: Epitope in DE loop
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (196)..(206)
: OTHER INFORMATION: Epitope in FG loop
US-09-949-375A-2

Query Match 55.8%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.9e-98;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 FTPTVKILQSSCGGHHFPTIOLCLVSGYTPGTINITIWLLEDQYMDVLDLSTASTOE 309
:
:
:
DB 4 FTPTVKILQSSCGGHHFPTIOLCLVSGYTPGTINITIWLLEDQYMDVLDLSTASTOE 63
:
:
:
OY 310 GELASTOSELTLSQKHWLSDRTYTCQVYGGHTEFEDSTKCADSNPBGVAYLSRPSFD 369
:
:
:
DB 64 GELASTOSELTLSQKHWLSDRTYTCQVYGGHTEFEDSTKCADSNPBGVAYLSRPSFD 123
:
:
:
OY 370 LFIKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEEQRNGTLTVSTLPVGT 429
:
:
:
DB 124 LFIKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEEQRNGTLTVSTLPVGT 183
:
:
:
OY 430 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPVYAFATPEWPGSDKRTLACLIO 489
:
:
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DB 184 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPVYAFATPEWPGSDKRTLACLIO 243
:
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:
OY 490 NFMEDISVOMLHNEVOLDPARHSTTOPRRTKSGGFFVFSRLLEVTRAEMWOKDEFICRAV 549
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DB 244 NFMEDISVOMLHNEVOLDPARHSTTOPRRTKSGGFFVFSRLLEVTRAEMWOKDEFICRAV 303
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OY 550 HEAASPSQTVORAVSNPGK 569
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DB 304 HEAASPSQTVORAVSNPGK 323
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RESULT 12
US-09-949-375A-4
; Sequence 4, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3
US-09-949-375A-4

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Query Match	55.8%;	Score 1707;	DB 9;	Length 323;
Best Local Similarity	100.0%;	Pred. No. 8.9e-98;		
Matches 320;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	250	FPPPYKIIQSSCDGGHPPIIOLLCIVSGTPTINITYLEGOVWVDVLSASTJOE	309
Db	4	FPPPYKIIQSSCDGGHPPIIOLLCIVSGTPTINITYLEGOVWVDVLSASTJOE	63
OY	310	GELASTQSELTLSQKHWLSDRYYTCQVITYQCHTEBDSTKCCADSNPRGVSAIYLSRPSFD	369
Db	64	GELASTQSELTLSQKHWLSDRYYTCQVITYQCHTEBDSTKCCADSNPRGVSAIYLSRPSFD	123
OY	370	LFRKSPITITCLVVDLAPSKGTYNLTWRSRASKPVNHSTREKROKNTLTVSTLTVGT	429
Db	124	LFRKSPITITCLVVDLAPSKGTYNLTWRSRASKPVNHSTREKROKNTLTVSTLTVGT	183
OY	430	RDWIEBETTYQCRVTHPLRPALMRSTYTSQGPRAAEVYAFATPBMFGSRDKRTLACLIQ	489
Db	184	RDWIEBETTYQCRVTHPLRPALMRSTYTSQGPRAAEVYAFATPBMFGSRDKRTLACLIQ	243
OY	490	NFMPEBISQWMLHNEQVLPDARHSTQPRKTSQSFVFSRLEYLATWMEQKDEFFICRAV	549
Db	244	NFMPEBISQWMLHNEQVLPDARHSTQPRKTSQSFVFSRLEYLATWMEQKDEFFICRAV	303
OY	550	HEAASPSQTVQRAVSVNPGK	569
Db	304	HEAASPSQTVQRAVSVNPGK	323

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RESULT 13
US-09-949-375A-6
? Sequence 6, Application US/09949375A
? Patent No. US20020172673A1
? GENERAL INFORMATION:
? APPLICANT: KLYSNER, Steen et al.
? TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
? FILE REFERENCE: 3631-0111P
? CURRENT APPLICATION NUMBER: US/09/949,375A
? CURRENT FILING DATE: 2002-01-18
? NUMBER OF SEQ ID NOS: 38
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 6
? LENGTH: 323
? TYPE: PRT
? ORGANSIM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5
US-09-949-375A-6

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Query Match      55.8%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.9e-98;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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QY	250	ETPEPTKIIQSSODGGGHPPTIOLLCVSGTPEITINITMLEGQVWDVDSIASTTQE	309
Db	4	ETPEPTKIIQSSODGGGHPPTIOLLCVSGTPEITINITMLEGQVWDVDSIASTTQE	63
QY	310	GELASTQSELTLSOKHMLSDRTTYCOVTVYQGHTEFDSIKKCADSNPRGSAYLSRPSFD	369
Db	64	GELASTQSELTLSOKHMLSDRTTYCOVTVYQGHTEFDSIKKCADSNPRGSAYLSRPSFD	122
QY	370	LFIRKSPITTCVLVDLAPSKGTVNLTWNASRKPVNHSTREKORNGTLTAVSTLPEVT	428
Db	124	LFIRKSPITTCVLVDLAPSKGTVNLTWNASRKPVNHSTREKORNGTLTAVSTLPEVT	183
QY	430	RDMEGETTQCRVTHPLHPLMRSTTKTSGCPRAPEYAFATPEMPSRDKRTLACLIQ	488
Db	184	RDMEGETTQCRVTHPLHPLMRSTTKTSGCPRAPEYAFATPEMPSRDKRTLACLIQ	243
QY	490	NFMPEDISVQMLHNEVQLPDARHSTTQPRKKTGSGEFVFSRLRYTRAMBEKQDEFCIRAV	549
Db	244	NFMPEDISVQMLHNEVQLPDARHSTTQPRKKTGSGEFVFSRLRYTRAMBEKQDEFCIRAV	303
QY	550	HEAASPQTVQRAVSVPGR	569
Db	304	HEAASPQTVQRAVSVPGR	323

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RESULT 14
US-10-176-664-1
Sequence 1, Application US/10176664
Publication No. US20030031663A1
GENERAL INFORMATION:
APPLICANT: Helliman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER.: US/10/176,664
CURRENT FILING DATE: 2002-06-19
PRIORITY APPLICATION NUMBER: US/09/401,636
PRIORITY FILING DATE: 1999-09-22
PRIORITY APPLICATION NUMBER: US 60/106,652
PRIORITY FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 331
Type: PRT
ORGANISM: Artificial Sequence.
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-1

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Query Match	55.8%;	Score 1707;	DB 9;	Length 331;
Best Local Similarity	100.0%;	Pred. No. 9.1e-98;		
Matches 320;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	250	FFPPTVAILIOSCGDGGHPPPTLOLLICLVSGYTPGINTINTEWEDQVMDVLSASTQOE	308
Db	12	FTPTVAILIOSCGDGGHPPPTLOLLICLVSGYTPGINTINTEWEDQVMDVLSASTQOE	71
QY	310	GELASTQSELTLSOKHMLSDRTYTCVYQGHTEFEDSTKKCADSNPRVSAVLSNPSPD	366
Db	72	GELASTQSELTLSOKHMLSDRTYTCVYQGHTEFEDSTKKCADSNPRVSAVLSNPSPD	133
QY	370	LFTRKSTTTCCLVVDLAPSKGYNLTWMSAASKPVMHSTRKEKORNGTLVYSTRLPGT	422
Db	132	LFTRKSTTTCCLVVDLAPSKGYNLTWMSAASKPVMHSTRKEKORNGTLVYSTRLPGT	19
QY	430	RDWIEGETYQCRVTHPLPRALMRSTTKTSGPRAAEVYAFATPEMPSRDKRTLACLIQ	488
Db	192	RDWIEGETYQCRVTHPLPRALMRSTTKTSGPRAAEVYAFATPEMPSRDKRTLACLIQ	25
QY	490	NFMEDISVQVMLNEVQDLPARHSTTQPKRTKSGGFVNSRLSEVTRAEMBEOKDEFICAV	54
Db	252	NFMEDISVQVMLNEVQDLPARHSTTQPKRTKSGGFVNSRLSEVTRAEMBEOKDEFICAV	31

OY 550 HEASPSQTVORAVSNPGK 569
|||||
Db 312 HEASPSQTVORAVSNPGK 331

RESULT 15

US-10-207-655-329
; Sequence 329, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 329
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-329

Query Match 55.8%; Score 1707; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 9.1e-98;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 FTPTPVKILQSSCDGGHPPTIQLCLVSGTPTGTTNITWLEDQVMDVDLSTASTQOE 309
|||||
Db 8 FTPTPVKILQSSCDGGHPPTIQLCLVSGTPTGTTNITWLEDQVMDVDLSTASTQOE 67
|||||
OY 310 GELASTQSELISQKHMLSDRTYTCQVYOGHTFEDSTKCKADSNPRGVSATLSRPSPD 369
|||||
Db 68 GELASTQSELISQKHMLSDRTYTCQVYOGHTFEDSTKCKADSNPRGVSATLSRPSPD 127
|||||
OY 370 LFIRKSPITTCIVDLAPSKGTVINLTWSRASKPVNHSTREKORNGTLVTVSTLPVGT 429
|||||
Db 128 LFIRKSPITTCIVDLAPSKGTVINLTWSRASKPVNHSTREKORNGTLVTVSTLPVGT 187
|||||
OY 430 RDMIGETVOCRVTPHLPALMRSTKTSGRAPAEVYAFATPEWPGSRDKRTIACLIQ 489
|||||
Db 188 RDMIGETVOCRVTPHLPALMRSTKTSGRAPAEVYAFATPEWPGSRDKRTIACLIQ 247
|||||
OY 490 NFMPEDISVOMLHNEVQLPDARHSTTOPRKTGSGFFVFSRLVETRAEMQKDEFICRAV 549
|||||
Db 248 NFMPEDISVOMLHNEVQLPDARHSTTOPRKTGSGFFVFSRLVETRAEMQKDEFICRAV 307
|||||
OY 550 HEASPSQTVORAVSNPGK 569
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Db 308 HEASPSQTVORAVSNPGK 327

Search completed: July 15, 2003, 07:17:20
Job time : 44.6521 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:55:24 ; Search time 22.8412 Seconds
(without alignments)
732.958 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDKHTHCPCAPPELL.....HEAASPSQTVQRAVSNPGK 569

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1273.5	41.6	711	4	US-09-485-737B-90
2	1232	40.3	660	4	US-09-181-706-8
3	1232	40.3	660	4	US-09-458-791-8
4	1232	40.3	660	4	US-09-459-066-8
5	1225	40.0	232	2	US-08-595-043A-50
6	1225	40.0	331	4	US-09-178-869-2
7	1225	40.0	360	4	US-09-180-100-11
8	1225	40.0	371	1	US-08-236-311-7
9	1225	40.0	371	3	US-08-457-918-7
10	1225	40.0	376	4	US-09-180-100-22
11	1225	40.0	396	2	US-08-784-512-3
12	1225	40.0	396	4	US-09-176-228-3
13	1225	40.0	424	5	PCT-US95-03866-12
14	1225	40.0	424	5	PCT-US95-03866-14
15	1225	40.0	437	5	PCT-US96-10043-11
16	1225	40.0	442	5	PCT-US96-10043-9
17	1225	40.0	446	3	US-08-397-411-7
18	1225	40.0	449	1	US-08-458-516-13
19	1225	40.0	459	1	US-08-157-101A-7
20	1225	40.0	476	2	US-08-378-939-10
21	1225	40.0	476	3	US-08-487-550-4
22	1225	40.0	478	3	US-08-487-550-12
23	1225	40.0	478	3	US-08-487-550-8
24	1220	39.9	254	2	US-08-284-391B-33
25	1220	39.9	254	4	US-09-218-950-33
26	1220	39.9	389	4	US-09-131-247-14
27	1219	39.8	330	4	US-09-301-593-22

28	1219	39.8	451	2	US-08-887-352B-14	Sequence 14, Appl
29	1219	39.8	451	2	US-08-887-352B-16	Sequence 16, Appl
30	1219	39.8	451	2	US-08-887-352B-18	Sequence 18, Appl
31	1219	39.8	451	3	US-08-466-151-65	Sequence 65, Appl
32	1219	39.8	451	3	US-09-109-207C-14	Sequence 14, Appl
33	1219	39.8	451	4	US-09-109-207C-16	Sequence 16, Appl
34	1219	39.8	451	4	US-09-109-207C-18	Sequence 18, Appl
35	1219	39.8	451	4	US-09-282-505-2	Sequence 2, Appl
36	1219	39.8	451	4	US-09-054-255-2	Sequence 2, Appl
37	1219	39.8	451	4	US-09-296-005-14	Sequence 14, Appl
38	1219	39.8	451	4	US-09-296-005-16	Sequence 16, Appl
39	1219	39.8	451	4	US-09-296-005-18	Sequence 18, Appl
40	1219	39.8	452	3	US-09-027-449-71	Sequence 71, Appl
41	1219	39.8	452	4	US-09-026-985-71	Sequence 71, Appl
42	1219	39.8	452	4	US-09-121-952A-71	Sequence 71, Appl
43	1219	39.8	452	4	US-09-234-340A-71	Sequence 71, Appl
44	1219	39.8	453	3	US-08-466-151-8	Sequence 8, Appl
45	1219	39.8	453	4	US-08-466-163B-8	Sequence 8, Appl

ALIGNMENTS

```
RESULT 1
US-09-485-737B-90
Sequence 90, Application US/09485737B
Patent No. 6350860
GENERAL INFORMATION:
APPLICANT: Bayse, Marie-Ange
INVENTOR: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90
LENGTH: 711
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90
Query Match 41.6%; Score 1273.5; DB 4; Length 711;
Best Local Similarity 50.1%; Pred. No. 2.5e-99;
Matches 286; Conservative 45; Mismatches 109; Indels 131; Gaps 16;
1 EPKSCDKHTHCPCAPPELLGSPVFLPPPKDTLMSRPEVVCVVVDVSHEDPEVK 60
236 EPKSCDKHTHCPCAPPELLGSPVFLPPPKDTLMSRPEVVCVVVDVSHEDPEVK 295
61 NWYDGVGVHNYKTPREEDQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIKT 120
236 NWYDGVGVHNYKTPREEDQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIKT 355
121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOENNKKTP 180
356 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOENNKKTP 415
181 PYLDVGSEFFLYSKLTVDKSRMOQGNVSCSYMHALHNHYQOBSLSPGKVEGGGSG 240
416 PYLDVGSEFFLYSKLTVDKSRMOQGNVSCSYMHALHNHYQOBSLSPGKVEGGGSG 468
241 GGGSGGGSPFPYVKIIQSSCD---GGGHPPTIQLCLVSGTPTINTWLED--- 293
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Db 469 -----GGGS-----QVQLVQSGSELKKRGA-----SVKISKASGTYFTTDYGMNWKQAPG 514
QY 294 -----GQMDVD-----ISTASTQGGELASTQSELTLISQKHWLSDRT 331
Db 515 QGLAMGMNINTYESTESTYDFKGRFVSLDTSVSAALQISSLKAEQY-----AT 565
QY 332 YTC-----QVLYGHFTFEDSTKKCADSNPRGVSATVLSRPPDLFIKSPPTITCLVVDL 385
Db 566 YFCARRGTYANDYMG-----QGTIVTVSSGGSGGGGGSDIVLTQSPA----- 613
QY 386 APSKGYVLTWMSRAGKPVNSTRKEKORNGTLTVSTLPGTRDMWIEGETYOCRVTHP 445
Db 614 -----TMSASPERGV-----TLTCSASSISYWFVYHQRPGS----- 646
QY 446 HLPALMRSTK-TSGPRAPEVYAFATPEWPGSRDKRTLACLIONFPEDISVQWMLNE 504
Db 647 --PILLIYDTSNLASGVA-----RFGSGSGTSYSLTISRMEPEDFATYFCHOS 694
QY 505 VOLPDARHSTQPRKTKSGGFVFSRLVTR 535
Db 695 SSYP-----FTFGG-----TKLEIKR 711

RESULT 2
US-09-181-706-8
: Sequence 8, Application US/09181706
: Patent No. 6130068
: GENERAL INFORMATION:
: APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
: APPLICANT: Robert F. Dubose, Richard S. Johnson
: TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Janis C. Henry
: STREET: 51 University St.
: CITY: Seattle
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC-compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/181,706
: FILING DATE: October 28, 1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/958,598 (converted to a
: APPLICATION NUMBER: Provisional, see below)
: FILING DATE: October 28, 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
: APPLICATION NUMBER: conversion to Provisional application)
: FILING DATE: October 26, 1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Henry, Janis C
: REGISTRATION NUMBER: 34,347
: REFERENCE/DOCKET NUMBER: 2631-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)470-4189
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 660 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-181-706-8

Query Match 40.3%; Score 1232; DB 4; Length 660;
Best Local Similarity 93.0%; Pred. No. 7.2e-96;
Matches 227; Conservative 7; Mismatches 8; Indels 2; Gaps 1;
QY 1 EPKSGDKHPCPPAPAPELLGSPSYFLPPPKKOTLMSTRPEVTCVYVDVSHDPEYK 60
Db 32 DKRSCDKHTPCPPAPAPAGAPSVFLPPPKKOTLMSTRPEVTCVYVDVSHDPEYK 91
QY 61 NMVYDGEVHNVKRPREEQYNSTRVYVSVTLVHONMNGKREYCKVSNALPAPIEKT 120
Db 92 NMVYDGEVHNAKRPREEQYNSTRVYVSVTLVHODMLNGKREYCKVSNALPAPIEKT 151
QY 121 ISKAKVQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 180
Db 152 ISKAKQPREQVYTLPPSRREEMTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 211
QY 181 PVLDSVGSFFLYSKLTVDKSRMOGNGVSCSVMEHALHNHYOQSLSPKVGSGSG 240
Db 212 PVLDSGGSFFLYSKLTVDKSRMOGNGVSCSVMEHALHNHYOQSLSPKVGSGSG 269
QY 241 GGGS 244
Db 270 GGGS 273

RESULT 3
US-09-458-791-8
: Sequence 8, Application US/09458791
: Patent No. 6174689
: GENERAL INFORMATION:
: APPLICANT: Spriggs, Melanie
: TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Janis C. Henry
: STREET: 51 University St.
: CITY: Seattle
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: MS-DOS/Windows 95
: SOFTWARE: word for windows 95, 7.0a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/458,791
: FILING DATE: 10-Dec-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/958,598
: FILING DATE: 28-OCT-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Henry, Janis C
: REGISTRATION NUMBER: 34,347
: REFERENCE/DOCKET NUMBER: 2631
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)470-4189
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 661 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-458-791-8

Query Match 40.3%; Score 1232; DB 4; Length 660;
Best Local Similarity 93.0%; Pred. No. 7.2e-96;
Matches 227; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

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QY      1  EPKSCKTHPCPCPADELGGSPFELPPKCKOTLMSRPEYTCVYVDSHDEPVKF  60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      32 DKRSCKTHPCPCPADELGGSPFELPPKCKOTLMSRPEYTCVYVDSHDEPVKF  91

QY      61 NMVYDGEVHNATKREBOYNSTRVYSVLTVLHQNMNNGKEYCKVSKNALPAPIEKT  120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      92 NMVYDGEVHNATKREBOYNSTRVYSVLTVLHQDLNNGKEYCKVSKNALPAPIEKT  151

QY      121 ISKAKYQRPBPQYTLTPSRDELFTNOVSLTCLVNGGFPSDIAEMESNGPENNYTTP  180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      152 ISKAKQRPBPQYTLTPSRDEEMTNOVSLTCLVNGGFPSDIAEMESNGPENNYTTP  211

QY      181 PVLDSGSEFFLYSKLTVDKSRMQQGNVSCSYMHBALNHHYQOBSLSLSPCKYVGGGSG  240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      212 PVLDSGSEFFLYSKLTVDKSRMQQGNVSCSYMHBALNHHYQOBSLSLSPCK  269

QY      241 GGGG 244
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Db      270 GGGG 273

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RESULT 4
US-09-459-066-8
; Sequence 8, Application US/09459066
Date of issue 010500

APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-459-066-8

Query Match	40.3%	Score 1232	DB 4	Length 660
Best Local Similarity	93.0%	Pred. No. 7.2e-96		
Matches 227; Conservative	7;	Mismatches 8;	Indels 2;	Gaps 1;

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Oy      1 EPKSCCKHTCTCPAPELLGGSVFLEPPPKPKDTLMISRTPEVTCVVWDVSHEDEYVKF   60
          : ::::::::::::::::::::|::::::::::::::::::::::::::::::::::::|
Db     32 DKRSCDKTHTCTPCPAPEAGASVFLFPKPCKDTLMIISTPEVTICVVDVSHEDYEKF   91
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OY	6	NWVVDGVEHNVNTRKREDOYNSTFRVSVLTVLHQNMNNGKEKCKVSNKALPAPLEKT	120
Dd	92	NMYVDGEVHNNAKTKFREDOYNSTRVSVLTVLHQDLNKGERTCKVSNKALPAPLEKT	151
OY	121	ISAKAYOPREPQYYTLTPSPRDELITRNQVSLTCLVGCFPSDIAEWESNCGPENNYKTTY	180
Dd	152	ISAKAGPREPQYYTLTPSPREMETKNQVSLTCLVGCFPSDIAEWESNCGPENNYKTTY	211
OY	181	PVLDVSQSFPLYSKLTVDKSRMOQGNVWSCSYMHALNNHYQQNSLSLPCKVGGGGSG	240
Dd	212	PVLDVSQSFPLYSKLTVDKSRMOQGNVWSCSYMHALNNHYTKOQLSLSPCK - GGGGSG	269
OY	241	GGGS 244	
Dd	270	GGGS 273	

RESULT 5
US-08-595-043A-50
; Sequence 50, Application US/08595043A

```

1 GENERAL INFORMATION:
2 APPLICANT: SGARLATO, GREGORY D.
3 TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
4 NUMBER OF SEQUENCES: 90
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: MEDLEN & CARROLL
7 STREET: 220 MONTGOMERY STREET, SUITE 2200
8 CITY: SAN FRANCISCO
9 STATE: CALIFORNIA
10 COUNTRY: UNITED STATES OF AMERICA
11 ZIP: 94104
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/595,043A
20 FILING DATE: 31-JAN-1996
21 CLASSIFICATION: 435
22
23 ATTORNEY/AGENT INFORMATION:
24 NAME: CARROLL, PETER G.
25 REGISTRATION NUMBER: 32,837
26 REFERENCE/DOCKET NUMBER: SGAR-00371
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (415) 705-8410
29 TELEFAX: (415) 397-8338
30
31 INFORMATION FOR SEQ ID NO: 50:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 232 amino acids
34 TYPE: amino acid
35 TOPOLOGY: linear
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37 MOLECULE TYPE: protein
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Query Match	40.0%	Score 1225	DB 2	Length 232
Best Local Similarity	97.0%	Pred.No. 6e-96		
Matches 225	Conservative	3	Mismatches 4	Indels 0
				Gaps 0

Db
61 NWYDGEVHNATKPREQYNSTYRVSVLIVHQNMNGCKEYCKSNALAPLEIKT 120
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Ey
61 NWYDGEVHNATKPREQYNSTYRVSVLIVHQNMNGCKEYCKSNALAPLEIKT 120
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Db 121 ISKAGQPREQVYITLPSSRDELTKNOVSLTCLVKGFPDIAVWESNGQENNKKTP 1800

Db 181 PVLDSGSEFLYKLTVDKSRMOGNNFSCSVMHDLNHNHYOKSLSPGK 232

RESULT 6

US-09-178-869-2

Sequence 2, Application US/091788698
Patent No. 6197294
GENERAL INFORMATION:
APPLICANT: Tao, Meng
APPLICANT: Wong, Shou
APPLICANT: Hickey, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/178, 869B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-09-178-869-2

Query Match 40.0%; Score 1225; DB 4; Length 331;
Best Local Similarity 97.0%; Pred. No. 1e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHNCPCPAPPELLGGSVFLPPPKKDTLMISRPEVTCVAVDVSHDDPEVKF 60
Db 100 EPKSCDTHNCPCPAPPELLGGSVFLPPPKKDTLMISRPEVTCVAVDVSHDDPEVKF 159
Qy 61 NMVYDGEVHNHVKTRPREQYNSTYRVYSLTVLHOMMNGKEVKCKYSNKALEPIEKT 120
Db 160 NMVYDGEVHNHVKTRPREQYNSTYRVYSLTVLHOMMNGKEVKCKYSNKALEPIEKT 219
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNOVSLTCLVKGFEYPSDIAVWESNGOPENNYKTP 180
Db 220 ISKAKGPREQVYTLPPSRDELTKNOVSLTCLVKGFEYPSDIAVWESNGOPENNYKTP 279
Qy 181 PVLDSGSEFLYKLTVDKSRMOGNNFSCSVMHDLNHNHYOKSLSPGK 232
Db 280 PVLDSGSEFLYKLTVDKSRMOGNNFSCSVMHDLNHNHYOKSLSPGK 331

RESULT 7

US-09-180-100-11

Sequence 11, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180, 100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-100-11

Query Match 40.0%; Score 1225; DB 4; Length 360;
Best Local Similarity 97.0%; Pred. No. 1.2e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHNCPCPAPPELLGGSVFLPPPKKDTLMISRPEVTCVAVDVSHDDPEVKF 60

Db 129 EPKSCDTHNCPCPAPPELLGGSVFLPPPKKDTLMISRPEVTCVAVDVSHDDPEVKF 188

RESULT 8

US-08-236-311-7

Sequence 7, Application US/08236311
Patent No. 556335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236, 311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28, 616
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-236-311-7

Query Match 40.0%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 1.2e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHNCPCPAPPELLGGSVFLPPPKKDTLMISRPEVTCVAVDVSHDDPEVKF 60

Db 140 EPKSCDKHTHTCPPCAPAPELLGSPSVFLPPPKKDTLMSRPEVTCVAVDVSHDEPEVKF 199
Qy 61 NMVYDGEVHNHVKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKYNNKALPAPIEKT 120
Db 200 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKYNNKALPAPIEKT 259
Qy 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYWESNGOPENNYKTTTP 180
Db 260 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYWESNGOPENNYKTTTP 319
Qy 181 PVLDSVGSFELYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 232
Db 320 PVLDSGSEFLYSLKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 371

RESULT 9
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kuhnec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-7

Query Match 40.0%; Score 1225; DB 3; length 371;
Best Local Similarity 97.0%; Pred. No. 1.2e-95;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKHTHTCPPCAPAPELLGSPSVFLPPPKKDTLMSRPEVTCVAVDVSHDEPEVKF 60
Db 140 EPKSCDKHTHTCPPCAPAPELLGSPSVFLPPPKKDTLMSRPEVTCVAVDVSHDEPEVKF 199
Qy 61 NMVYDGEVHNHVKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKYNNKALPAPIEKT 120
Db 200 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKYNNKALPAPIEKT 259
Qy 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYWESNGOPENNYKTTTP 180
Db 260 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYWESNGOPENNYKTTTP 319
Qy 181 PVLDSVGSFELYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 232
Db 320 PVLDSGSEFLYSLKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 371

RESULT 10
US-09-180-100-22
; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-22

Query Match 40.0%; Score 1225; DB 4; length 376;
Best Local Similarity 97.0%; Pred. No. 1.2e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKHTHTCPPCAPAPELLGSPSVFLPPPKKDTLMSRPEVTCVAVDVSHDEPEVKF 60
Db 145 EPKSCDKHTHTCPPCAPAPELLGSPSVFLPPPKKDTLMSRPEVTCVAVDVSHDEPEVKF 204
Qy 61 NMVYDGEVHNHVKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKYNNKALPAPIEKT 120
Db 205 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLHQNMMNGKEYCKYNNKALPAPIEKT 264
Qy 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYWESNGOPENNYKTTTP 180
Db 265 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYWESNGOPENNYKTTTP 324
Qy 181 PVLDSVGSFELYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 232
Db 325 PVLDSGSEFLYSLKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 376

RESULT 11
US-08-784-512-3
; Sequence 3, Application US/08784512
; Patent No. 5872209
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BUETNER, Frank
; APPLICANT: CATTERSON, Bruce
; APPLICANT: HUGHES, Clare
; TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
; TITLE OF INVENTION: and native aggrecan to study the proteolytic activity of

TITLE OF INVENTION: "Aggrecanase" in cell culture systems
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396
US-08-784-512-3

Query Match 40.0%; Score 1225; DB 2; Length 396;
Best Local Similarity 97.0%; Pred. No. 1.3e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDTHTCPCPAPBELLGSPVFLPPPKDITLMSRTPEVTCVVDVSHDPEYKF 60
DB 165 EPKSCDTHTCPCPAPBELLGSPVFLPPPKDITLMSRTPEVTCVVDVSHDPEYKF 224
QY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMMNGKEKCKVSNKALPAPIEKT 120
DB 225 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMMNGKEKCKVSNKALPAPIEKT 284
QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 180
DB 285 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 344
QY 181 PVLDVGSFELYSKLTVDKSRMOGQNVFSCSVMEHALHNHYTKSLSPCK 232
DB 345 PVLDSDGSFELYSKLTVDKSRMOGQNVFSCSVMEHALHNHYTKSLSPCK 396
RESULT 12
US-09-176-228-3
Sequence 3, Application US/09176228
GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENMUELLER, Bernd
APPLICANT: BUETTNER, Frank
APPLICANT: CATERSON, Bruce
APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: and native aggrecan to study the proteolytic activity of
TITLE OF INVENTION: "Aggrecanase" in cell culture systems

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/176,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396
US-09-176-228-3

Query Match 40.0%; Score 1225; DB 4; Length 396;
Best Local Similarity 97.0%; Pred. No. 1.3e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDTHTCPCPAPBELLGSPVFLPPPKDITLMSRTPEVTCVVDVSHDPEYKF 60
DB 165 EPKSCDTHTCPCPAPBELLGSPVFLPPPKDITLMSRTPEVTCVVDVSHDPEYKF 224
QY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMMNGKEKCKVSNKALPAPIEKT 120
DB 225 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMMNGKEKCKVSNKALPAPIEKT 284
QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 180
DB 285 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 344
QY 181 PVLDVGSFELYSKLTVDKSRMOGQNVFSCSVMEHALHNHYTKSLSPCK 232
DB 345 PVLDSDGSFELYSKLTVDKSRMOGQNVFSCSVMEHALHNHYTKSLSPCK 396
RESULT 13
PCT-0595-03866-12
Sequence 12, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocke, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave

STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-03866-12

Query Match 40.0%; Score 1225; DB 5; Length 424;
Best Local Similarity 97.0%; Pred. No. 1.5e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKRDKTLMISRPEVTCVYVDVSHEDPEVKF 60
DB 193 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKRDKTLMISRPEVTCVYVDVSHEDPEVKF 252
QY 61 NMVYDGVENVHVKTKPREEOYNSTRVYSVLTVLHONMMNGKEYCKSNKALPAPIEKT 120
DB 253 NMVYDGVENVHVKTKPREEOYNSTRVYSVLTVLHODMLNGKEYCKSNKALPAPIEKT 312
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNYKTP 180
DB 313 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNYKTP 372
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQORSLSLSPGK 232
DB 373 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQORSLSLSPGK 424

RESULT 14
PCT-US95-03866-14
Sequence 14, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: Cytomed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-03866-14

Query Match 40.0%; Score 1225; DB 5; Length 424;
Best Local Similarity 97.0%; Pred. No. 1.5e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKRDKTLMISRPEVTCVYVDVSHEDPEVKF 60
DB 193 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKRDKTLMISRPEVTCVYVDVSHEDPEVKF 252
QY 61 NMVYDGVENVHVKTKPREEOYNSTRVYSVLTVLHONMMNGKEYCKSNKALPAPIEKT 120
DB 253 NMVYDGVENVHVKTKPREEOYNSTRVYSVLTVLHODMLNGKEYCKSNKALPAPIEKT 312
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNYKTP 180
DB 313 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNYKTP 372
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQORSLSLSPGK 232
DB 373 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSVMEHALNHNHYQORSLSLSPGK 424

RESULT 15
PCT-US96-10043-11
Sequence 11, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Iech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-11

Query Match 40.0%; Score 1225; DB 5; Length 437;
Best Local Similarity 97.0%; Pred. No. 1.5e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY	1	EPKSCDKTHTCPGCPAPPELLGGPSVFLP	PPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF	60
DB	206	EPKSCDKTHTCPGCPAPPELLGGPSVFLP	PPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF	265
QY	61	NWYVDGVEVHNAKTKRPREQYNSTIRRV	SVLTIVLHQMNGKEIKCKVSNKALPAPIEKT	120
DB	266	NWYVDGVEVHNAKTKRPREQYNSTIRRV	SVLTIVLHQMNGKEIKCKVSNKALPAPIEKT	325
QY	121	ISKAKVQPREPVYTLPPSRDELTKNOVSL	TCLVKGFYPSDIAVEMESNGQPENNYKTTP	180
DB	326	ISKAKVQPREPVYTLPPSRDELTKNOVSL	TCLVKGFYPSDIAVEMESNGQPENNYKTTP	385
QY	181	PVLDSVGSFFLYSKLTVDKSRMQQGNVFS	CSVMHEALHNHYQOQSLSLSPGK	232
DB	386	PVLDSVGSFFLYSKLTVDKSRMQQGNVFS	CSVMHEALHNHYQOQSLSLSPGK	437

Search completed: July 15, 2003, 07:02:42
Job time : 23.8412 secs